

## SEQUENCE LISTING

<110> GROSJEAN-COURNOYER, Marie-Claire  
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 LEBRUN, Marc-Henri  
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<120> Mutagenesis of *Aspergillus* fungi and identification  
 of genes essential for growth

<130> 346 723 - US

<150> PCT/IB 03/01 374

<151> 2003-03-13

<150> US 60/363 543

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<170> PatentIn Ver. 3.2

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<213> *Aspergillus fumigatus*

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His Thr Glu Val Leu Asn Thr Leu Asp Ser Asp Gly Arg Ile Phe Val
      85              90              95

```

```

Ala Ser Val Ser Pro Gln Val Arg Ala Ser Leu Ala Ala Thr Tyr Gly
      100             105             110

```

```

Ile Thr Glu Arg Glu Ala Lys Tyr Met Ile Asp Gln Phe Leu Met Gly
      115             120             125

```

```

Pro His Gly Leu Arg Ala Gly Gly Lys His Gly Asn Gly Phe Thr Trp
      130             135             140

```

Val	Val	Asp	Thr	Asn	Val	Met	Arg	Glu	Ala	Val	Leu	Ala	Leu	Thr	Ala	145	150	155	160
Asp	Glu	Val	Thr	Ser	Ser	Leu	Leu	Ser	Thr	Gly	Ser	Gly	Ser	Leu	Pro	165	170	175	
Lys	Ser	Pro	Ile	Leu	Ser	Ser	Ala	Cys	Pro	Gly	Trp	Ile	Cys	Tyr	Ala	180	185	190	
Glu	Lys	Thr	His	Pro	Phe	Ile	Leu	Pro	His	Leu	Ser	Arg	Leu	Lys	Ser	195	200	205	
Pro	Gln	Ala	Leu	Ser	Gly	Thr	Phe	Leu	Lys	Ser	Val	Leu	Ser	Lys	Ala	210	215	220	
Leu	Gly	Val	Pro	Pro	Ser	Gln	Ile	Trp	His	Leu	Ala	Ile	Met	Pro	Cys	225	230	235	240
Phe	Asp	Lys	Lys	Leu	Glu	Ala	Ser	Arg	Glu	Glu	Leu	Thr	Asp	Ile	Ala	245	250	255	
Trp	Ala	Ser	Thr	Phe	Thr	Gln	Ser	Gln	Thr	Thr	Pro	Val	Arg	Asp	Val	260	265	270	
Asp	Cys	Val	Ile	Thr	Thr	Arg	Glu	Leu	Leu	Thr	Leu	Ala	Thr	Ala	Arg	275	280	285	
Gly	Leu	Ser	Leu	Pro	Asn	Leu	Pro	Leu	Lys	Pro	Leu	Pro	Ala	Ser	Cys	290	295	300	
Leu	Thr	Pro	Phe	Pro	Asp	Gln	Ala	Leu	Glu	Ser	Phe	Leu	Phe	Ser	Lys	305	310	315	320
Ser	Ser	Ser	Gly	Gln	Thr	Val	Glu	Ser	Gly	Thr	Ser	Gly	Gly	Tyr	Leu	325	330	335	
His	His	Val	Leu	Gln	Ile	Phe	Gln	Ala	Arg	Asn	Pro	Gly	Ser	Lys	Ile	340	345	350	
Val	Thr	Gln	Arg	Gly	Arg	Asn	Ala	Asp	Val	Val	Glu	Tyr	Val	Leu	Met	355	360	365	
Ser	Ser	Gly	Asp	Glu	Pro	Leu	Phe	Arg	Ala	Ala	Arg	Tyr	Tyr	Gly	Phe	370	375	380	
Arg	Asn	Ile	Gln	Asn	Leu	Val	Arg	Lys	Leu	Lys	Pro	Ala	Arg	Val	Ser	385	390	395	400
Arg	Leu	Pro	Gly	Ala	Lys	Pro	Gln	Ala	Val	Ser	Ser	Ser	Ala	Asn	Arg	405	410	415	
Arg	Gln	Pro	Met	Ser	Arg	Asn	Ala	Ala	Pro	Ala	Gly	Thr	Gly	Ala	Asp	420	425	430	
Tyr	Ala	Tyr	Val	Glu	Val	Met	Ala	Cys	Pro	Gly	Gly	Cys	Thr	Asn	Gly	435	440	445	
Gly	Gly	Gln	Ile	Arg	Ile	Glu	Asp	Ala	Arg	Glu	Ala	Val	Pro	Asn	Ala	450	455	460	

Leu Lys Glu Thr Ser Thr Glu Thr Pro Val Ala Ala Pro Lys Pro Thr  
465 470 475 480

Pro His Glu Gln Arg Ala Trp Leu Ala Arg Val Asp Glu Ala Tyr Tyr  
485 490 495

Ser Ala Asp Ser Asp Ser Glu Gly Ser Val Thr Thr Glu Pro Val Ser  
500 505 510

Val Leu Ser Arg Asp Asn Gln Ile His Glu Phe Leu Asn Tyr Trp Ser  
515 520 525

Glu Lys  
530

<210> 7

<211> 942

<212> DNA

<213> *Aspergillus fumigatus*

<400> 7

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actgggaagt cgaccttgct caagagactc ttcgctgaat accccgatac ttctgattta 180
tccgtgtctc gtacgtctaa ccccttgcca accctcattg actatgcctg cgaattgttt 240
cttttggtgg aattgcgctg aacgggtgtt gttatattta gataccactc gagctccccg 300
tcccggggaa gaaaatggac gtgagtatta cttcacaact aaagaagatt tcctggatct 360
tgtgagcaag aatgccttta tcgagcatgc gcagtttggt ggcaattact acggtactac 420
tgtgcaggca gtgaaggatg ttgcgcagaa gggcaagatc tgcgttctcg acattgagat 480
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gaagaactag agaaaagact gcgtgggaga gcaaccgaga ctgaggagag cttgacggta 720
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gattggattg tcgacggtgg taactttgga gcgcgtcaat ga 942
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<210> 8

<211> 600

<212> DNA

<213> *Aspergillus fumigatus*

<400> 8

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gtgtctcata ccaactcgagc tcccgcgtcc gggaagaaa atggacgtga gtattacttc 180
acaactaaag aagatttcct ggatcttggt agcaagaatg cttttatcga gcatgcgcag 240
tttggtggca attactacgg tactactgtg caggcagtga aggatgttgc gcagaagggc 300
aagatctgcg ttctcgacat tgagatgagg ggcgtgaaac aagtcaagcg caccgatctt 360
gatgctcgat tcttattttt agcaccctcc tcccttgaag aactagagaa aagactgcgt 420
gggagagcaa ccgagactga ggagagcttg acgaaacgcc ttgccaagc taaaaatgaa 480
ttggaatatg cggcgcagcc tggtctcat gataagattg tcgtgaacga tgacctggag 540
aaggcttata aggaactgcg ggattggatt gtcgacggtg gtaactttgg agcgcgtcaa 600
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<210> 9

<211> 200

&lt;212&gt; PRT

<213> *Aspergillus fumigatus*

&lt;400&gt; 9

Met Thr Thr Gly Ala Val Gln Arg Phe Arg Pro Val Val Val Ser Gly  
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Pro Ser Gly Thr Gly Lys Ser Thr Leu Leu Lys Arg Leu Phe Ala Glu  
 20 25 30

Tyr Pro Asp Thr Phe Asp Leu Ser Val Ser His Thr Thr Arg Ala Pro  
 35 40 45

Arg Pro Gly Glu Glu Asn Gly Arg Glu Tyr Tyr Phe Thr Thr Lys Glu  
 50 55 60

Asp Phe Leu Asp Leu Val Ser Lys Asn Ala Phe Ile Glu His Ala Gln  
 65 70 75 80

Phe Gly Gly Asn Tyr Tyr Gly Thr Thr Val Gln Ala Val Lys Asp Val  
 85 90 95

Ala Gln Lys Gly Lys Ile Cys Val Leu Asp Ile Glu Met Arg Gly Val  
 100 105 110

Lys Gln Val Lys Arg Thr Asp Leu Asp Ala Arg Phe Leu Phe Leu Ala  
 115 120 125

Pro Pro Ser Leu Glu Glu Leu Glu Lys Arg Leu Arg Gly Arg Ala Thr  
 130 135 140

Glu Thr Glu Glu Ser Leu Thr Lys Arg Leu Ala Gln Ala Lys Asn Glu  
 145 150 155 160

Leu Glu Tyr Ala Ala Gln Pro Gly Ser His Asp Lys Ile Val Val Asn  
 165 170 175

Asp Asp Leu Glu Lys Ala Tyr Lys Glu Leu Arg Asp Trp Ile Val Asp  
 180 185 190

Gly Gly Asn Phe Gly Ala Arg Gln  
 195 200

&lt;210&gt; 10

&lt;211&gt; 2059

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;400&gt; 10

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 cttggttgga tcgacaaact cttggataat gtttcgacca tattcatcga cttatataag 360  
 gatgagctaa ggagcacacg ggctaggatt attgagtacc cattcgataa gtacttcgac 420  
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 gagatcaacg agagaaagga ccctcttgct tcatcagata acggcgggcc acctccgcca 540  
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cctcgattac	tccgcccccg	cagatggtga	ggacgcaccg	gctcctgtag	tcgaggctgt	960
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&lt;210&gt; 11

&lt;211&gt; 1923

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;400&gt; 11

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gttcgagcgc	agaatcaggc	agcagcagc	gcagctccta	tctacaagaa	ggaaaagtat	180
actctgaaat	ggaagcaagt	aaaggatttc	aatctgatat	ttgtggctgt	atatcaatct	240
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tacttcgacc	agcaggtcgc	agagcttgag	gacaatgctg	gggtcctac	atcagaatct	420
ctcgtagtag	agatcaacga	gagaaaggac	cctcttgtct	catcagataa	cggcgggcca	480
cctccgccac	ccgtgcctgt	tgcgcagggc	gtggcgacct	cggacgaggg	ttcgccaccc	540
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catgctcgca	atttgaagg	acttagtacc	cgggagaaatg	ctggagaggt	tgaactctac	1500
gagaagggat	atggaaagga	tgacgcgaat	gtagcgaagg	atgcagtgga	gtacgggtgcg	1560
gcgaatcatt	tcgacgttgt	gttgattgat	actgccggtc	gccgtcataa	cgaccaacgc	1620
cttatgtctt	cgctcgagaa	gttcgccaag	ttcgccaaac	cagataagat	cttcatggtc	1680

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aag 1923

```

<210> 12

<211> 641

<212> PRT

<213> *Aspergillus fumigatus*

<400> 12

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Met Leu Glu Ala Phe Glu Val Leu Thr Thr Ser Gly Val Val Leu Trp
  1             5             10             15

```

```

Ser Lys Ser Tyr Ala Pro Val Gly Ala His Val Val Asn Ser Leu Ile
          20             25             30

```

```

Asn Asp Val Phe Ile Glu Glu Lys Val Arg Ala Gln Asn Gln Ala Ala
      35             40             45

```

```

Ser Ser Ala Ala Pro Ile Tyr Lys Lys Glu Lys Tyr Thr Leu Lys Trp
      50             55             60

```

```

Lys Gln Val Lys Asp Phe Asn Leu Ile Phe Val Ala Val Tyr Gln Ser
      65             70             75             80

```

```

Leu Leu His Leu Gly Trp Ile Asp Lys Leu Leu Asp Asn Val Ser Thr
          85             90             95

```

```

Ile Phe Ile Asp Leu Tyr Lys Asp Glu Leu Arg Ser Thr Arg Ala Arg
          100             105             110

```

```

Ile Ile Glu Tyr Pro Phe Asp Lys Tyr Phe Asp Gln Gln Val Arg Glu
      115             120             125

```

```

Leu Glu Asp Asn Ala Gly Ala Pro Thr Ser Glu Ser Leu Val Val Glu
      130             135             140

```

```

Ile Asn Glu Arg Lys Asp Pro Leu Val Ser Ser Asp Asn Gly Gly Pro
      145             150             155             160

```

```

Pro Pro Pro Pro Val Pro Val Ala Gln Gly Val Ala Thr Ser Asp Glu
          165             170             175

```

```

Gly Ser Pro Pro Gln Thr Pro Asp Leu Ser Arg Ser Ser Thr Pro Ile
          180             185             190

```

```

Ser Gly His Leu Leu Thr Ala Lys Gly Gly Pro Ala Gly Arg Ala Ser
      195             200             205

```

```

Arg Arg Ala Arg Lys Ala Ala Asn Ala Ser Ala Thr Ala Ser Ser Gly
      210             215             220

```

```

Asp Glu Ser Ile Arg Lys Gly Lys Thr Leu Lys Ser Gly Lys Lys Met
      225             230             235             240

```

```

Arg Lys Trp Asp Ala Asp Gly Phe Ala Asp Glu Asp Asp Gly Lys Val
          245             250             255

```



Leu Asp Tyr Ser Ala Pro Ala Asp Gly Glu Asp Ala Pro Ala Pro Val  
 260 265 270  
 Val Glu Ala Val Ala Gln Glu Ser Trp Gly Arg Arg Thr Gly Lys Gly  
 275 280 285  
 Gln Phe Val Leu Lys Asp Leu Gly Asp Glu Val His Ser Ile Leu Glu  
 290 295 300  
 Asn Ala Asp His Glu Lys Thr Lys Ser Ser Ser Thr Gly Phe Val  
 305 310 315 320  
 Gly Ser Gly Val Asn Ala Leu Gly Gly Phe Phe Arg Asn Ile Val Gly  
 325 330 335  
 Gly Lys Val Leu Thr Glu Ala Asp Leu Glu Lys Pro Leu Lys Ala Met  
 340 345 350  
 Glu Asp His Leu Leu Lys Lys Asn Val Ala Arg Glu Ala Ala Val Arg  
 355 360 365  
 Leu Cys Gln Gly Val Gln Arg Glu Leu Val Gly Lys Lys Thr Gly Asn  
 370 375 380  
 Phe Gln Ser Val Asp Ala Ala Leu Arg Ser Ala Met Glu Ser Ser Leu  
 385 390 395 400  
 Arg Lys Ile Leu Thr Pro Thr Ser Ser Leu Asp Leu Leu Arg Glu Ile  
 405 410 415  
 Asp Ala Val Arg Ser Pro Thr Ser Lys Gly Gln Ala Pro Arg Pro Tyr  
 420 425 430  
 Val Ile Ser Ile Val Gly Val Asn Gly Val Gly Lys Ser Thr Asn Leu  
 435 440 445  
 Gly Lys Ile Cys Tyr Phe Leu Leu Gln Asn Asn Tyr Arg Val Leu Ile  
 450 455 460  
 Ala Ala Cys Asp Thr Phe Arg Ser Gly Ala Val Glu Gln Leu Arg Val  
 465 470 475 480  
 His Ala Arg Asn Leu Lys Glu Leu Ser Thr Arg Glu Asn Ala Gly Glu  
 485 490 495  
 Val Glu Leu Tyr Glu Lys Gly Tyr Gly Lys Asp Ala Ala Asn Val Ala  
 500 505 510  
 Lys Asp Ala Val Glu Tyr Gly Ala Ala Asn His Phe Asp Val Val Leu  
 515 520 525  
 Ile Asp Thr Ala Gly Arg Arg His Asn Asp Gln Arg Leu Met Ser Ser  
 530 535 540  
 Leu Glu Lys Phe Ala Lys Phe Ala Lys Pro Asp Lys Ile Phe Met Val  
 545 550 555 560  
 Gly Glu Ala Leu Val Gly Thr Asp Ser Val Met Gln Ala Arg Asn Phe  
 565 570 575  
 Asn Gln Ala Phe Gly Thr Gly Arg Asn Leu Asp Gly Phe Ile Ile Ser

580	585	590
Lys Cys Asp Thr Val Gly Asp Met Val Gly Thr Leu Val Ser Met Val		
595	600	605
His Ala Thr Gly Ile Pro Ile Val Phe Leu Gly Val Gly Gln His Tyr		
610	615	620
Gly Asp Leu Arg Gly Leu Ser Val Pro Trp Ala Val Asn Leu Leu Met		
625	630	635
		640

Lys

<210> 13  
 <211> 1564  
 <212> DNA  
 <213> *Aspergillus fumigatus*

<400> 13

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aaattatggg	ctgacctaga	aggtgctcta	acctactgaa	cttctacgtt	aatatgctaa	180
tattaattgg	tagctcgagg	atataacctc	gacttcgaat	cccccaagaa	tgacaagctc	240
agcctgttcg	aactcggaga	ccgagttctac	gaccacatgc	ttctcctgcc	tcccaagtca	300
aagggttagc	gttaccctta	gacatgtcca	tatgtctctgc	tttgtacatc	tcaattgacc	360
tcttggccag	gctatggacc	ctcccttacc	cccaagaata	tcattgattt	catgaacaag	420
gacggtaacg	tctctctcgc	cttgtcgggc	aagtccacaa	ccgccagcgc	tatcagctcg	480
ctgctattgg	agctcgatct	ccatctccct	gtcgatcggt	cctctgtcac	cgctgatcac	540
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ggcaagttga	ggtccgatac	caaggctttc	tttgatggcg	agggcgttgt	agcatttccc	660
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gatggtgaaa	tcactcccga	gaagctgaac	cctaagatct	atcgaataaa	gaatgaaact	1080
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 <211> 1380  
 <212> DNA  
 <213> *Aspergillus fumigatus*

<400> 14

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aaattatggg	ctgacctaga	aggatataac	ctcgacttcg	aatcccccaa	gaatgacaag	180
ctcagcctgt	tcgaactcgg	agaccgagtc	tacgaccaca	tgcttctcct	gcctcccaag	240

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```

<210> 15

<211> 460

<212> PRT

<213> *Aspergillus fumigatus*

<400> 15

```

Met Arg Trp Cys Leu Thr Leu Leu Ala Phe Cys Phe Leu Ala Val Val
  1              5              10              15

```

```

Arg Ala Leu Ser Ser Ser Gly Ser Arg Leu Leu Val Val Leu Glu Asp
      20              25              30

```

```

Ala Thr Glu Lys Glu Leu Tyr Ser Lys Leu Trp Ala Asp Leu Glu Gly
      35              40              45

```

```

Tyr Asn Leu Asp Phe Glu Ser Pro Lys Asn Asp Lys Leu Ser Leu Phe
      50              55              60

```

```

Glu Leu Gly Asp Arg Val Tyr Asp His Met Leu Leu Leu Pro Pro Lys
      65              70              75              80

```

```

Ser Lys Gly Tyr Gly Pro Ser Leu Thr Pro Lys Asn Ile Ile Asp Phe
      85              90              95

```

```

Met Asn Lys Asp Gly Asn Val Leu Leu Ala Leu Ser Gly Lys Ser Thr
      100             105             110

```

```

Thr Ala Ser Ala Ile Ser Ser Leu Leu Leu Glu Leu Asp Leu His Leu
      115             120             125

```

```

Pro Val Asp Arg Ser Ser Val Thr Val Asp His Phe Asn Tyr Asp Thr
      130             135             140

```

```

Leu Ser Ala Ser Asp Lys His Asp Val Leu Leu Leu His Arg Pro Gly
      145             150             155             160

```

```

Lys Leu Arg Ser Asp Thr Lys Ala Phe Phe Asp Gly Glu Gly Val Val
      165             170             175

```

Ala Phe Pro Arg Ala Val Pro His Thr Leu Gly Asp Ala Asn Pro Leu

180						185						190					
Ile	Ala	Pro	Ile	Leu	Arg	Ala	Pro	Ala	Thr	Ala	Tyr	Ser	Tyr	Asn	Pro		
195						200						205					
Lys	Glu	Asp	Ala	Ser	Ser	Val	Glu	Asp	Val	Ala	Ala	Thr	Gly	Ser	Gln		
210						215						220					
Leu	Ala	Leu	Val	Ser	Ala	Met	Gln	Ala	Arg	Asn	Ser	Ala	Arg	Phe	Thr		
225						230						235					
Leu	Leu	Gly	Ser	Val	Glu	Ser	Leu	Gln	Asp	Gln	Trp	Phe	Ser	Ala	Thr		
245						250						255					
Val	Lys	Ala	Pro	Gly	Asp	Gly	Lys	Gln	Met	Lys	Thr	Val	Asn	Gln	Glu		
260						265						270					
Phe	Ala	Lys	Gln	Leu	Thr	Ala	Trp	Thr	Phe	Lys	Glu	Thr	Gly	Val	Leu		
275						280						285					
Lys	Val	Gly	Lys	Ile	Glu	His	His	Leu	Ala	Glu	Asp	Gly	Glu	Ile	Thr		
290						295						300					
Pro	Glu	Lys	Leu	Asn	Pro	Lys	Ile	Tyr	Arg	Ile	Lys	Asn	Glu	Thr	Val		
305						310						315					
Phe	Ser	Ile	Glu	Leu	Ser	Glu	Tyr	Asn	Tyr	Asp	Arg	Tyr	Ala	Pro	Phe		
325						330						335					
Glu	Val	Pro	Thr	Gly	Asp	Ala	Val	Gln	Leu	Glu	Phe	Thr	Met	Leu	Ser		
340						345						350					
Pro	Phe	His	Arg	Leu	Asn	Leu	Glu	Pro	Val	Arg	Arg	Thr	Asp	Asn	Ser		
355						360						365					
Thr	Val	Tyr	Ser	Thr	Arg	Phe	Thr	Thr	Pro	Asp	Gln	His	Gly	Ile	Phe		
370						375						380					
Ser	Phe	Arg	Val	Asn	Tyr	Lys	Arg	Pro	Phe	Leu	Thr	Asn	Ile	Glu	Glu		
385						390						395					
Lys	Leu	Glu	Val	Thr	Val	Arg	His	Phe	Ala	His	Asn	Glu	Tyr	Pro	Arg		
405						410						415					
Ser	Trp	Lys	Ile	Ser	Gly	Gly	Trp	Val	Trp	Ile	Ala	Gly	Leu	Trp	Ser		
420						425						430					
Val	Ile	Ala	Gly	Phe	Leu	Val	Phe	Val	Val	Ala	Trp	Leu	Tyr	Ser	Ala		
435						440						445					
Pro	Ser	Ala	Ala	Ala	Leu	Asn	Thr	Lys	Lys	Thr	Gln						
450						455						460					

&lt;210&gt; 16

&lt;211&gt; 2376

&lt;212&gt; DNA

&lt;213&gt; Aspergillus fumigatus

&lt;400&gt; 16

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cctgctgaga	tctttcgtcg	tcggttacgc	tctctcgacg	gccgacattg	ccctttgggg	480
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&lt;210&gt; 17

&lt;211&gt; 2145

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;400&gt; 17

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```

&lt;210&gt; 18

&lt;211&gt; 715

&lt;212&gt; PRT

<213> *Aspergillus fumigatus*

&lt;400&gt; 18

```

Met Ser Gln Tyr Gln Leu Thr Val Ala Thr Arg Ala Asn Gln Pro Tyr
  1              5              10              15

```

```

Val Leu Pro Val Leu Leu Val Ala Thr Ser Ile Asn Glu Ala Arg Pro
      20              25              30

```

```

Ser Pro Val Ile Ser Ile Thr Tyr Glu Asp Thr Ala Val Leu Arg Glu
      35              40              45

```

```

Gly Asp Lys Ala Val Val Gln Tyr Thr Gly Ala Ser Gly Asn Pro Ile
      50              55              60

```

```

Phe Gly Leu Ile Asn Ala Val Gln Glu Leu Arg Lys Asp Phe Pro Phe
      65              70              75              80

```

```

Leu Asn Ser Lys Asp Glu Lys Leu Glu Asn Glu Trp Leu Ser Gln Leu
      85              90              95

```

```

Glu Ala Phe Ala Pro Leu Asp Phe Lys Ala Leu Asp Pro Glu Leu Gln
      100             105             110

```

```

Arg Leu Asp Thr His Leu Leu Leu Arg Ser Phe Val Val Gly Tyr Ala
      115             120             125

```

```

Leu Ser Thr Ala Asp Ile Ala Leu Trp Gly Ala Ile Arg Gly Asn Arg
      130             135             140

```

```

Val Ala Val Ala Ala Ile Lys Lys Gly Ser Leu Val Asn Val Thr Arg
      145             150             155             160

```

Trp Phe Tyr Phe Leu Glu Asp Leu Cys Pro Trp Ala Thr Ser Thr Leu  
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 Glu Val Leu Asn Gln Ala Val Arg Glu Lys Lys Ala Ala Lys Ala Lys  
 180 185 190  
 Glu Gly Ala Ser Tyr Asp Ile Ala Leu Leu Asn Thr Glu Lys Gly Val  
 195 200 205  
 Val Thr Arg Phe Pro Pro Glu Pro Ser Gly Tyr Leu His Ile Gly His  
 210 215 220  
 Ala Lys Ala Ala Leu Leu Asn Asp Tyr Phe Ala His Glu Lys Tyr Asn  
 225 230 235 240  
 Gly Thr Leu Leu Val Arg Phe Asp Asp Thr Asn Pro Ser Asn Glu Lys  
 245 250 255  
 Leu Glu Phe Gln Asp Ala Ile Ile Glu Asp Leu Ala Leu Met Gly Ile  
 260 265 270  
 Lys Pro Asp Lys Met Ser Tyr Thr Ser Asp Tyr Phe Asp Glu Leu Tyr  
 275 280 285  
 Gln Tyr Ala Leu Gln Ile Ile Lys Asp Gly Asn Ala Tyr Ala Asp Asp  
 290 295 300  
 Thr Glu Lys Glu Val Met Ala Glu Gln Arg Met Asn Gly Lys Pro Ser  
 305 310 315 320  
 Lys Arg Arg Asp Ala Ser Val Glu Glu Asn Leu Ala Arg Phe Glu Glu  
 325 330 335  
 Met Lys Lys Gly Thr Pro Glu Gly Leu Arg Trp Cys Ile Arg Ala Lys  
 340 345 350  
 Met Ser Val Asp Asn Pro Asn Lys Ala Met Arg Asp Pro Val Ile Tyr  
 355 360 365  
 Arg Cys Asn Pro Ala Pro His His Arg Thr Gly Thr Lys Trp Lys Ile  
 370 375 380  
 Tyr Pro Thr Tyr Asp Phe Ala Cys Pro Ile Val Asp Ser Ile Glu Gly  
 385 390 395 400  
 Val Thr His Ala Leu Arg Thr Ile Glu Tyr Arg Asp Arg Asn Pro Gln  
 405 410 415  
 Tyr Gln Trp Phe Leu Asp Thr Leu Lys Leu Arg His Val Gln Ile Trp  
 420 425 430  
 Asp Phe Ala Arg Met Asn Phe Ile Arg Thr Leu Leu Ser Lys Arg Lys  
 435 440 445  
 Leu Thr Lys Leu Val Asn Gln Gly Val Val Trp Gly Trp Asp Asp Pro  
 450 455 460  
 Arg Phe Pro Thr Ile Arg Gly Ile Arg Arg Arg Gly Met Thr Ile Pro  
 465 470 475 480  
 Ala Leu Arg Glu Phe Ile Leu Lys Gln Gly Pro Ser Lys Asn Ile Thr

485					490					495					
Asn	Leu	Asp	Trp	Thr	Leu	Ile	Trp	Ala	Thr	Asn	Lys	Lys	Tyr	Ile	Asp
500					505					510					
Pro	Val	Ala	Pro	Arg	His	Thr	Ala	Ile	Leu	Lys	Lys	Asp	Met	Val	Lys
515					520					525					
Ala	Ile	Val	Lys	Gly	Gly	Pro	Ala	Thr	Pro	Tyr	Thr	Glu	Glu	Lys	Pro
530					535					540					
Lys	His	Gly	Lys	Asn	Pro	Ala	Val	Gly	Met	Lys	Lys	Val	Val	Phe	Gly
545					550					555					
Asn	Thr	Val	Ile	Phe	Asp	Gln	Lys	Asp	Ala	Lys	Ser	Phe	Lys	Gln	Asp
565					570					575					
Glu	Glu	Ile	Thr	Leu	Met	Ser	Trp	Gly	Asn	Ala	Ile	Val	Arg	Lys	Ile
580					585					590					
Glu	Thr	Asp	Pro	Thr	Ser	Gly	Ile	Val	Lys	Glu	Leu	Glu	Leu	Glu	Leu
595					600					605					
His	Leu	Glu	Gly	Asp	Phe	Lys	Lys	Thr	Glu	Lys	Lys	Val	Thr	Trp	Leu
610					615					620					
Ser	Thr	Glu	Gly	Gln	Asp	Leu	Ile	Pro	Val	Glu	Leu	Val	Asp	Phe	Asp
625					630					635					
Tyr	Leu	Leu	Asn	Lys	Asp	Thr	Leu	Gln	Glu	Asp	Asp	Val	Leu	Glu	Asp
645					650					655					
Val	Leu	Asn	Lys	Asn	Thr	Glu	Phe	Arg	Glu	Asp	Ala	Val	Ala	Asp	Cys
660					665					670					
Asn	Val	Ala	Glu	Leu	Lys	Glu	Gly	Asp	Ile	Ile	Gln	Phe	Glu	Arg	Lys
675					680					685					
Gly	Tyr	Tyr	Arg	Val	Asp	Arg	Ala	Tyr	Val	Pro	Gly	Lys	Pro	Ala	Val
690					695					700					
Leu	Phe	Asn	Ile	Pro	Thr	Gly	Lys	Thr	Gly	Lys					
705					710					715					

&lt;210&gt; 19

&lt;211&gt; 2639

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;400&gt; 19

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&lt;212&gt; PRT

<213> *Aspergillus fumigatus*

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Val Leu Gln Leu Ser Asp Arg Val Asn Glu Leu Asn Ser Leu His Gly  
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Asp Pro Glu Asp Pro Leu Trp Ile Ser Leu Leu Asn Cys Leu Gly Ser  
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<210> 26

<211> 1479

<212> DNA

<213> *Aspergillus fumigatus*



&lt;400&gt; 26

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ccgtccttga cgatcaatta cgaggcaacg caggatcttg attctaccaa tgcttttgaa 120
gggtccagaga aactcttgga ggtgtgggtc ggccttccg ctcaggaatt aggtccagcg 180
cagcccgccg gtctgaaggc tgttccggag gagatctgga aggacatgtt ggatctcgtc 240
aattgccagg tcctctcgat tgtttcgtca gaggatgtgg acgcctacct gctctccgag 300
tctagcatgt tcgtttggcc tcacaaactc atcttgaaga cttgtggtac caccactctt 360
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aagaacttcc tgttccccga ccgccagcgg ggccctcacc gcagctggag agatgaagtg 540
cggactatgg ataagctctt cctcaacggc agcgccata tgattggcaa gatgaatggc 600
gagcactggg acttgtacct gactgaacct cataccatgc tcaccccgcc aacgagcccg 660
ggagccaaga ccgagtttac ggaaacggag accaagggtc tcagtgtacc ccagggcgct 720
gctctgcaga ctgattcgga ggatgagact ttggaagtct tgatgaccga cttggatgag 780
gagaacgcca agcagttcta cctcgagaat gccactgccg ttgcggagaa ccgttatcgc 840
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cggattgtcc acgacctcga cggctatgag cttgtcttcc gctattatga acgcctggac 1440
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&lt;210&gt; 27

&lt;211&gt; 493

&lt;212&gt; PRT

<213> *Aspergillus fumigatus*

&lt;400&gt; 27

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Met Val Tyr Ile Gly Ile Pro Lys Asn Tyr Thr Ala Ser Pro Ser Ser
 1             5             10             15

Phe Ala Gly Thr Pro Ser Leu Thr Ile Asn Tyr Glu Ala Thr Gln Asp
      20             25             30

Leu Asp Ser Thr Asn Ala Phe Glu Gly Pro Glu Lys Leu Leu Glu Val
      35             40             45

Trp Phe Ala Pro Ser Ala Gln Glu Leu Gly Pro Ala Gln Pro Ala Gly
      50             55             60

Leu Lys Ala Val Pro Glu Glu Ile Trp Lys Asp Met Leu Asp Leu Val
      65             70             75             80

Asn Cys Gln Val Leu Ser Ile Val Ser Ser Glu Asp Val Asp Ala Tyr
      85             90             95

Leu Leu Ser Glu Ser Ser Met Phe Val Trp Pro His Lys Leu Ile Leu
      100            105            110

Lys Thr Cys Gly Thr Thr Thr Leu Leu Ser Gly Leu Pro Arg Ile Leu
      115            120            125

Glu Ile Ala Ala Leu Phe Gly Gly Phe Pro Lys Ser Thr Ala Pro Ser
      130            135            140

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Arg Gly Ile Ser Val Ala Ala Ala Pro Tyr Arg Val Phe Tyr Ser Arg  
 145 150 155 160  
 Lys Asn Phe Leu Phe Pro Asp Arg Gln Arg Gly Pro His Arg Ser Trp  
 165 170 175  
 Arg Asp Glu Val Arg Thr Met Asp Lys Leu Phe Leu Asn Gly Ser Ala  
 180 185 190  
 Tyr Met Ile Gly Lys Met Asn Gly Glu His Trp Tyr Leu Tyr Leu Thr  
 195 200 205  
 Glu Pro His Thr Met Leu Thr Pro Pro Thr Ser Pro Gly Ala Lys Thr  
 210 215 220  
 Glu Phe Thr Glu Thr Glu Thr Lys Val Leu Ser Val Pro Gln Gly Ala  
 225 230 235 240  
 Ala Leu Gln Thr Asp Ser Glu Asp Glu Thr Leu Glu Val Leu Met Thr  
 245 250 255  
 Asp Leu Asp Glu Glu Asn Ala Lys Gln Phe Tyr Leu Glu Asn Ala Thr  
 260 265 270  
 Ala Val Ala Glu Asn Arg Tyr Arg Asn Ser Asn Ser Glu Lys Ser Gly  
 275 280 285  
 His Val Asp Val Phe Ser Asn Thr Ser Ser Asp Ile Ser Asp Phe Asp  
 290 295 300  
 Ser Asp Gly Ser Gln Val Leu Pro Pro Glu Leu Thr Thr Glu Gly His  
 305 310 315 320  
 Ala Leu Gly Thr Val Val Ser Glu Ala Cys Gly Leu Ser Ser Val Tyr  
 325 330 335  
 Pro Lys Glu Lys Tyr Pro Asp Ser Arg Ile Asp Ala Tyr Leu Phe Thr  
 340 345 350  
 Pro Cys Gly Phe Ser Ala Asn Gly Val Ile Pro Pro Pro Glu Gly Lys  
 355 360 365  
 Ala Gly Thr His Tyr Phe Thr Val His Val Thr Pro Glu Pro His Cys  
 370 375 380  
 Ser Tyr Ala Ser Phe Glu Thr Asn Val Pro His Ser Gln Asn Gly Gln  
 385 390 395 400  
 Thr Thr Ala Gly Ile Ile Lys Gln Val Val Asp Ile Phe Lys Pro Gly  
 405 410 415  
 Arg Phe Ser Val Thr Leu Phe Glu Ala Lys Pro Ala Leu Ser Gln Val  
 420 425 430  
 Glu Asp Glu Trp Lys Glu Ala Lys Tyr Leu Ala Ala Arg Arg Thr Ala  
 435 440 445  
 Lys Met Glu His Val Glu Gly Tyr Arg Arg Val Asp Arg Ile Val His  
 450 455 460

Asp Leu Asp Gly Tyr Glu Leu Val Phe Arg Tyr Tyr Glu Arg Leu Asp  
 465 470 475 480

Trp Lys Gly Gly Ala Pro Arg Leu Gly Glu Glu Arg Ser  
 485 490

<210> 28

<211> 637

<212> DNA

<213> *Aspergillus fumigatus*

<400> 28

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agcccaaaaa gagtatcatt tctgacgaaa tgggtttttc ttcaatagac agtcaagagg 120
tccgccaaagg tcatcatcga gcgctactac cccaagttga cgctcgactt tgagaccaac 180
aagcgtcttt gcgatgagat cgctatcatt gcctccaagc gccttcgcaa caaggtgggc 240
aatccatcac tgagccgtac aacagtcgga atttgacttg ctgacgaaaa ctagattgct 300
ggttacacca cccaccttat gaagcgtatc cagcgtggcc ctgtccgcgg tatctcttc 360
aagctgcagg aggaggagcg tgagcgcaag gatcagtagg ttctgaggt ttccgctctg 420
gatgtttccc agaccgagtc cggccagctc gatgtcgatg ccgacaccaa ggaccttctc 480
aagtccatgg gcgtaagtcc tgttctcaac gcggttggtc gtgggtttta agcagtcctg 540
taacttatat tgcccactac agttcgacaa tctcaaggtc aacgttgtca acgtctcca 600
acatcagggt caggagcgcc cccgcgcgtt ccggtag 637

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<210> 29

<211> 417

<212> DNA

<213> *Aspergillus fumigatus*

<400> 29

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attgcctcca agcgccttcg caacaagatt gctgggttaca ccaccacct tatgaagcgt 180
atccagcgtg gccctgtccg cggatatctt ttcaagctgc aggaggagga gcgtgagcgc 240
aaggatcagt acgttcctga ggtttccgct ctggatgttt ccagaccga gtccggccag 300
ctcgatgtcg atgccgacac caaggacctt ctcaagtcca tgggcttcga caatctcaag 360
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```

<210> 30

<211> 139

<212> PRT

<213> *Aspergillus fumigatus*

<400> 30

Met Gly Arg Val Arg Thr Lys Thr Val Lys Arg Ser Ala Lys Val Ile  
 1 5 10 15

Ile Glu Arg Tyr Tyr Pro Lys Leu Thr Leu Asp Phe Glu Thr Asn Lys  
 20 25 30

Arg Leu Cys Asp Glu Ile Ala Ile Ile Ala Ser Lys Arg Leu Arg Asn  
 35 40 45

Lys Ile Ala Gly Tyr Thr Thr His Leu Met Lys Arg Ile Gln Arg Gly  
 50 55 60

Pro Val Arg Gly Ile Ser Phe Lys Leu Gln Glu Glu Glu Arg Glu Arg

65		70		75		80
Lys Asp Gln Tyr Val Pro Glu Val Ser Ala Leu Asp Val Ser Gln Thr						
	85			90		95
Glu Ser Gly Gln Leu Asp Val Asp Ala Asp Thr Lys Asp Leu Leu Lys						
	100			105		110
Ser Met Gly Phe Asp Asn Leu Lys Val Asn Val Val Asn Val Ser Gln						
	115			120		125
His Gln Val Gln Glu Arg Pro Arg Arg Phe Arg						
	130			135		

&lt;210&gt; 31

&lt;211&gt; 1035

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;400&gt; 31

atggcggttg	gaaagtatgc	caattcactt	ctattattgt	tctgaacgct	tttagcatgt	60
gtctggatac	ggtggtttac	aggtactgat	ccgggaacag	gaacaagcgc	ttgtcgaagg	120
gcaagaagg	tgtaagaag	aggaccgttg	atcctttctc	caggaaggac	gaatactctg	180
ttaaggtatg	tcgacgtgga	ctgtgtaagt	cgaccgcagc	taatctatat	caggcgcctt	240
ccactttcca	gatcagagag	tatgttgac	gcatatgatg	tcgaatgcag	gataaaggcg	300
attcacaatg	gtagtggaga	ttatgctgac	tgaattatag	tgctcggaag	actctgggtca	360
accgcaccag	tggtctcaag	aacgcacaatg	actccctgaa	gggtcgaatt	ttcgaggtct	420
cgctggctga	cctgcagaat	gatgaagacc	atgctttccg	caaggttaag	cttcgtgtgg	480
acgaggttca	gggcaagaac	tgtttgacca	acttccacgg	tcttgatttc	acaaccgaca	540
aattgcgatc	cctcgtgcgc	aagtggcagt	cgctgatcga	agccatgtca	ctgtgaagac	600
gaccgatgat	tatctccttc	ggctttttgc	tatcgcttc	accaagagac	gcccgaacca	660
gattaagaag	accacatatg	ctcgttcttc	tcaaatacgt	gccatccgca	agaagatgat	720
tgaaatcatg	cagagggagg	cagccagctg	ctctctcgct	cagctcactc	acaagctcat	780
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tgtgtgtgac	cctgttattc	ttactcgggg	tgaagactaa	ctgcaatcta	ggtccatatt	900
cgcaaggtca	agcttcttaa	ggctcccaag	ttcgacctgg	gtgcactgct	gaatctgcac	960
ggtgaatcta	caaccgatga	taagggccac	aaggctcgaga	gagagttaa	ggagcaggtt	1020
ctcgaaagcg	tttaa					1035

&lt;210&gt; 32

&lt;211&gt; 768

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;400&gt; 32

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agagatgtcg	ggaagactct	ggtcaaccgc	accagtggct	tcaagaacgc	caatgactcc	180
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cacggtcttg	atttcacaa	cgacaaattg	cgatccctcg	tgcgcaagtg	gcagtgcgtg	360
atcgaagcca	atgtcactgt	gaagacgacc	gatgattatc	tccttcggct	ttttgctatc	420
gccttcacca	agagacgccc	gaaccagatt	aagaagacca	catatgctcg	ttcttctcaa	480
atccgtgcca	tccgcaagaa	gatgattgaa	atcatgcaga	gggaggcagc	cagctgctct	540
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accaggga	tctatccttt	gcagaatgtc	catattcgca	aggtaagct	tcttaaggct	660
cccaagttcg	acctgggtgc	actgctgaat	ctgcacggtg	aatctacaac	cgatgataag	720
ggccacaagg	tcgagagaga	gttcaaggag	caggttctcg	aaagcggt		768

&lt;210&gt; 33

&lt;211&gt; 256

&lt;212&gt; PRT

<213> *Aspergillus fumigatus*

&lt;400&gt; 33

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Met Ala Val Gly Lys Asn Lys Arg Leu Ser Lys Gly Lys Lys Gly Val
 1          5          10          15

Lys Lys Arg Thr Val Asp Pro Phe Ser Arg Lys Asp Glu Tyr Ser Val
          20          25          30

Lys Ala Pro Ser Thr Phe Gln Ile Arg Asp Val Gly Lys Thr Leu Val
          35          40          45

Asn Arg Thr Ser Gly Leu Lys Asn Ala Asn Asp Ser Leu Lys Gly Arg
          50          55          60

Ile Phe Glu Val Ser Leu Ala Asp Leu Gln Asn Asp Glu Asp His Ala
65          70          75          80

Phe Arg Lys Val Lys Leu Arg Val Asp Glu Val Gln Gly Lys Asn Cys
          85          90          95

Leu Thr Asn Phe His Gly Leu Asp Phe Thr Thr Asp Lys Leu Arg Ser
          100          105          110

Leu Val Arg Lys Trp Gln Ser Leu Ile Glu Ala Asn Val Thr Val Lys
          115          120          125

Thr Thr Asp Asp Tyr Leu Leu Arg Leu Phe Ala Ile Ala Phe Thr Lys
          130          135          140

Arg Arg Pro Asn Gln Ile Lys Lys Thr Thr Tyr Ala Arg Ser Ser Gln
          145          150          155          160

Ile Arg Ala Ile Arg Lys Lys Met Ile Glu Ile Met Gln Arg Glu Ala
          165          170          175

Ala Ser Cys Ser Leu Ala Gln Leu Thr His Lys Leu Ile Pro Glu Val
          180          185          190

Ile Gly Arg Glu Ile Glu Lys Ala Thr Gln Gly Ile Tyr Pro Leu Gln
          195          200          205

Asn Val His Ile Arg Lys Val Lys Leu Leu Lys Ala Pro Lys Phe Asp
          210          215          220

Leu Gly Ala Leu Leu Asn Leu His Gly Glu Ser Thr Thr Asp Asp Lys
          225          230          235          240

Gly His Lys Val Glu Arg Glu Phe Lys Glu Gln Val Leu Glu Ser Val
          245          250          255

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<210> 34  
 <211> 614  
 <212> DNA  
 <213> *Aspergillus fumigatus*

<400> 34  
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 aatcatgtat atggacccat tttcccgtca ccagaagcaa ttatatgtaa gtgggtttttg 120  
 cttctggcgg aacggtcctg tgttgggaaa ttgacggcta tcaatagcgc ctgctaaacg 180  
 ggttatgtcc ctcaaagaac cgacgttgaa aatgtccaag tcccatgccg acagacgctc 240  
 aaggatcatt cttacggatt cgcccgcaga aatctccaaa aagatcaatg ctgcgctcac 300  
 agactcggaa ttaaccatta catatgaccc agtcgcgtcga cctggagtgg cgaatttaat 360  
 agagatcttg agtcacttcg atggacgaac ttgcgatgag attgccatgg aataccgttc 420  
 agccagtctt cgcgctctaa aggaacatct ggccagaacg ttgtccaatc atcttgagcc 480  
 aataagagag aagtatctct cactttagg agatcagact gactaccttg attctatagc 540  
 agaacagggg tctgaagccg cgcgggccaa cgctgaattg acaatggagc aagtcaaagt 600  
 cgctatgggc ttaa 614

<210> 35  
 <211> 552  
 <212> DNA  
 <213> *Aspergillus fumigatus*

<400> 35  
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 gttatgtccc tcaaagaacc gacgttgaaa atgtccaagt cccatgccga cagacgctca 180  
 aggatcattc ttacggattc gcccgcgaga atctccaaaa agatcaatgc tgcgctcaca 240  
 gactcggaat taaccattac atatgaccca gtccgctcgac ctggagtggc gaatttaata 300  
 gagatcttga gtcacttcga tggacgaact tgcgatgaga ttgccatgga ataccgttca 360  
 gccagtcttc gcgctctaaa ggaacatctg gccagaacgt tgtccaatca tcttgagcca 420  
 ataagagaga agtatctctc actttaggga gatcagactg actaccttga ttctatagca 480  
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 gctatgggct ta 552

<210> 36  
 <211> 184  
 <212> PRT  
 <213> *Aspergillus fumigatus*

<400> 36  
 Pro Val Gly Asp Asp Gln Arg Gln His Leu Glu Phe Ser Arg Asn Thr  
 1 5 10 15  
 Ala Asn Ser Phe Asn His Val Tyr Gly Pro Ile Phe Pro Ser Pro Glu  
 20 25 30  
 Ala Ile Ile Ser Pro Ala Lys Arg Val Met Ser Leu Lys Glu Pro Thr  
 35 40 45  
 Leu Lys Met Ser Lys Ser His Ala Asp Arg Arg Ser Arg Ile Ile Leu  
 50 55 60  
 Thr Asp Ser Pro Ala Glu Ile Ser Lys Lys Ile Asn Ala Ala Leu Thr  
 65 70 75 80  
 Asp Ser Glu Leu Thr Ile Thr Tyr Asp Pro Val Arg Arg Pro Gly Val  
 85 90 95

Ala Asn Leu Ile Glu Ile Leu Ser His Phe Asp Gly Arg Thr Cys Asp  
 100 105 110

Glu Ile Ala Met Glu Tyr Arg Ser Ala Ser Leu Arg Ala Leu Lys Glu  
 115 120 125

His Leu Ala Arg Thr Leu Ser Asn His Leu Glu Pro Ile Arg Glu Lys  
 130 135 140

Tyr Leu Ser Leu Val Gly Asp Gln Thr Asp Tyr Leu Asp Ser Ile Ala  
 145 150 155 160

Glu Gln Gly Ser Glu Ala Ala Arg Ala Asn Ala Glu Leu Thr Met Glu  
 165 170 175

Gln Val Lys Val Ala Met Gly Leu  
 180

<210> 37  
 <211> 819  
 <212> DNA  
 <213> *Aspergillus fumigatus*

<400> 37  
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 actcaggtac ggaactcgaa actacgctat aatgaggctt tactcgtgat ttggatgttg 120  
 acaataatgt tcctagaccg agagtctgtt tcacacctat gcgcagtatg catcgatgac 180  
 gaagctgcct ccgaaaccct cagaagaaga acaacggatt gaatcgcaac tgaaggatct 240  
 tcttgaaaag gtgtgcactt tgaggccctc tagtccagcc caacagacga tcatgctgac 300  
 acgatccgat catagcgtga agccctcatc tcccagctct cccgtctcct tgactccgaa 360  
 gccactctta ccgcatctgc cctgaaacag agcaatcttg cccgcaatcg cgaagtcttc 420  
 caggatcatc gccgcgaatt gcagcgcttg aacgccgcaa tcgccgagtc ccgcgaccga 480  
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 gcggctgagg cagactacat gctcgaggag cggggctgta tagatgaaaag ccataacatg 600  
 atagatgggtg tcctaagcca ggcgtatgca atcaacgaga gttttgggct acaacgtgaa 660  
 accctggcca gcatcaatcg ccgtatcgtc ggtgctgcca ataaggtacc aggaatgaat 720  
 gcattgattg gtaagattgg gacgaagagg agacgtgacg caatcatctt gggggctttc 780  
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<210> 38  
 <211> 681  
 <212> DNA  
 <213> *Aspergillus fumigatus*

<400> 38  
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 ccgaaaccct cagaagaaga acaacggatt gaatcgcaac tgaaggatct tcttgaaaag 180  
 cgtgaagccc tcatctccca gctctcccgct ctcttgact ccgaagccac tcttaccgca 240  
 tctgccctga aacagagcaa tcttgcccgc aatcgcgaa tcttccagga tcatcgccgc 300  
 gaattgcagc gcctgaacgc cgcaatcgcc gagtcccgcg accgagccaa tcttctgtct 360  
 aacgtccgct ccgacattga tgcctaccgc aattcaaacc ccgccgggc tgaggcagac 420  
 tacatgctcg aggagcgggg tcgtatagat gaaagccata acatgataga tgggtgtccta 480  
 agccaggcgt atgcaatcaa cgagagtttt gggctacaac gtgaaaccct ggccagcatc 540  
 aatcgccgta tcgtcgggtgc tgccaataag gtaccaggaa tgaatgcatt gattggtaag 600  
 attgggacga agaggagacg tgacgcaatc atcttggggg ctttcatcgg cttttgtttc 660  
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<210> 39  
 <211> 227  
 <212> PRT  
 <213> *Aspergillus fumigatus*

<400> 39  
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   1                  5                  10                  15  
 Arg Ser Leu Glu Thr Gln Thr Glu Ser Leu Phe His Thr Tyr Ala Gln  
           20                  25                  30  
 Tyr Ala Ser Met Thr Lys Leu Pro Pro Lys Pro Ser Glu Glu Glu Gln  
           35                  40                  45  
 Arg Ile Glu Ser Gln Leu Lys Asp Leu Leu Glu Lys Arg Glu Ala Leu  
           50                  55                  60  
 Ile Ser Gln Leu Ser Arg Leu Leu Asp Ser Glu Ala Thr Leu Thr Ala  
   65                  70                  75                  80  
 Ser Ala Leu Lys Gln Ser Asn Leu Ala Arg Asn Arg Glu Val Leu Gln  
                   85                  90                  95  
 Asp His Arg Arg Glu Leu Gln Arg Leu Asn Ala Ala Ile Ala Glu Ser  
           100                  105                  110  
 Arg Asp Arg Ala Asn Leu Leu Ser Asn Val Arg Ser Asp Ile Asp Ala  
           115                  120                  125  
 Tyr Arg Asn Ser Asn Pro Ala Ala Ala Glu Ala Asp Tyr Met Leu Glu  
   130                  135                  140  
 Glu Arg Gly Arg Ile Asp Glu Ser His Asn Met Ile Asp Gly Val Leu  
 145                  150                  155                  160  
 Ser Gln Ala Tyr Ala Ile Asn Glu Ser Phe Gly Leu Gln Arg Glu Thr  
           165                  170                  175  
 Leu Ala Ser Ile Asn Arg Arg Ile Val Gly Ala Ala Asn Lys Val Pro  
           180                  185                  190  
 Gly Met Asn Ala Leu Ile Gly Lys Ile Gly Thr Lys Arg Arg Arg Asp  
           195                  200                  205  
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 Phe Phe Arg  
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 <213> *Aspergillus fumigatus*

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<210> 41

<211> 1182

<212> DNA

<213> *Aspergillus fumigatus*

<400> 41

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<211> 394

<212> PRT

<213> *Aspergillus fumigatus*

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His	Glu	Ala	Ile	Asp	Leu	Ile	Ser	Ala	Leu	Leu	Glu	Tyr	Thr	Pro	Thr
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&lt;210&gt; 43

&lt;211&gt; 2209

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;400&gt; 43

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<210> 44  
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 <213> *Aspergillus fumigatus*

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 <211> 735  
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 <213> *Aspergillus fumigatus*

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 35 40 45

Phe Ile Lys Ser Met Trp Lys Ser Phe Lys Glu Lys His Ala Ser Lys  
 50 55 60  
 Phe Gly Gly Gly Ser Ala Glu Ala Ala Ala Ser Asp Gly Gly Gln Asp  
 65 70 75 80  
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 Val Ala Leu Ile Ala Gln Arg Met Arg Asp Gly Ile Glu Gln Asn Phe  
 100 105 110  
 Ser Asn Ala Pro Pro Ser Ser Gly Gln Ser Val Asn Tyr Glu Glu Lys  
 115 120 125  
 Arg Thr Gly Ser Leu Pro Gln Ser Thr Asp Ala Gln Glu Asp Gln Ser  
 130 135 140  
 Ser Ser Gly Ser Ala Ala Asn Gly Ser Arg Thr Asp Pro Gln Phe Lys  
 145 150 155 160  
 Asp Pro Glu Thr Ala Thr Cys Ala Leu Ser Lys Tyr Asp Asp Trp Arg  
 165 170 175  
 Asp Ser Val Leu Leu Arg Ile Gly Glu Val Val Asn Arg Asp Pro Glu  
 180 185 190  
 His Gly Glu Val Gln Ala Asn Glu Asn Pro Pro Ser Gly Gln Gln Ser  
 195 200 205  
 Gln Gln Ile Arg Ser Glu Glu Asp Asp Arg Ser Ile Arg Lys Leu Arg  
 210 215 220  
 Glu Val Phe Pro Pro Val Glu Thr Ser Leu Ser Gln Leu Pro Glu Ala  
 225 230 235 240  
 Lys Lys Leu Leu Ile Leu His Ser Leu Leu Leu Leu Val Leu Ser Leu  
 245 250 255  
 Glu His Tyr Asn Ala Trp Ser Arg Val Leu Met Leu Phe Val Thr Ser  
 260 265 270  
 Ser Leu Gly Leu Asp Val Lys Leu Leu Asn Glu Asp Glu Val Lys Val  
 275 280 285  
 Ala Arg Gly Leu Leu Asp Thr Ala Leu Ala Leu Ser Ser Asn Ala Pro  
 290 295 300  
 Arg Gln Asp Glu Ser Arg Ser Arg Asp Ser Ser Arg Lys Trp Lys Val  
 305 310 315 320  
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 340 345 350  
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 Gly Ser Gly Val Val Val Gly Gly Leu Phe Gly Ala Tyr Gly Gly Arg

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Ala	Leu	Glu	Glu	Ala	Ala	Leu	Glu	Ala	Lys	Asp	Arg	Arg	Gln	Glu	Gln
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Glu	Arg	Ala	His	Asn	Glu	Arg	Gln	Ala	Gly	Phe	Met	Gly	Glu	Gly	Arg
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<211> 510

<212> DNA

<213> *Aspergillus fumigatus*

<400> 46

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<212> DNA

<213> *Aspergillus fumigatus*

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ttg 423
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<210> 48

<211> 141

<212> PRT

<213> *Aspergillus fumigatus*

<400> 48

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1 5 10 15

Gly Arg Val Val Leu Ile Arg Ser Gly Pro Tyr Thr Gly Lys Leu Ala  
20 25 30

Ala Ile Val Glu Ile Ile Asp His Lys Arg Val Leu Val Asp Gly Pro  
35 40 45

Ser Thr Glu Glu Asn Lys Ile Val Pro Arg His Ala Leu Pro Leu Ala  
50 55 60

His Ala Thr Leu Thr Pro Phe Val Ile Pro Lys Leu Pro Arg Ala Ala

65	70	75	80
Gly Thr Gly Pro Val Lys Lys Leu Trp Glu Lys Asn Glu Ile Asp Gly			
	85	90	95
Lys Trp Ala Lys Ser Thr Ile Ala Gln Lys Thr Glu Arg Ala Glu Arg			
	100	105	110
Arg Lys Asn Leu Thr Asp Phe Glu Arg Phe Lys Val Leu Arg Leu Lys			
	115	120	125
Lys Gln Val Arg Ser Val Cys Glu Thr Met Gly Glu Leu			
	130	135	140

<210> 49  
 <211> 1413  
 <212> DNA  
 <213> *Aspergillus fumigatus*

<400> 49

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<210> 50  
 <211> 1284  
 <212> DNA  
 <213> *Aspergillus fumigatus*

<400> 50

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atcgctaagc	gcagaacccc	aaagatccaa	cggcaatact	cggatatttg	tggagggtca	360
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&lt;210&gt; 51

&lt;211&gt; 428

&lt;212&gt; PRT

<213> *Aspergillus fumigatus*

&lt;400&gt; 51

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Met Ala Leu Arg Arg Pro Leu Thr Leu Pro Arg His Ile Leu Asn Gly
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      20             25             30

Gly Gln Glu Gln Arg Lys Gly Leu Ala Thr Ala Val Pro Pro Val Thr
      35             40             45

Gln Asn Ala Ala Gly Ser Lys Gly Pro Thr Ala Met Val Phe Leu Asn
      50             55             60

Met Gly Gly Pro Ser Lys Ile Asp Glu Val Glu Asp Phe Leu Ser Arg
      65             70             75             80

Leu Phe Ala Asp Gly Asp Leu Ile Pro Leu Gly Arg Leu Gln Ser Tyr
      85             90             95

Leu Gly Pro Leu Ile Ala Lys Arg Arg Thr Pro Lys Ile Gln Arg Gln
      100            105            110

Tyr Ser Asp Ile Gly Gly Gly Ser Pro Ile Arg Lys Trp Ser Glu Tyr
      115            120            125

Gln Cys Glu Glu Met Cys Arg Leu Leu Asp Lys Ile Asn Pro Glu Thr
      130            135            140

Ala Pro His Lys Pro Tyr Val Ala Phe Arg Tyr Ala Asp Pro Leu Thr
      145            150            155            160

Glu Glu Met Tyr Thr Lys Leu Leu Glu Asp Gly Phe Gly Asn Gly Lys
      165            170            175

Gly Gly Arg Ala Val Ala Phe Thr Gln Tyr Pro Gln Tyr Ser Cys Ser
      180            185            190

Thr Thr Gly Ser Ser Leu Asn Glu Leu Trp Lys Trp Arg Thr Arg Leu
      195            200            205

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Glu Gly Lys Arg Ala Asn Gly Asn Met Asp Pro Ala Gly Ala Ile Gln  
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 Trp Ser Val Ile Asp Arg Trp Pro Thr His Pro Gly Leu Val Glu Ala  
 225 230 235 240  
 Phe Ala Arg Asn Ile Glu Glu Gln Leu Lys Thr Tyr Pro Glu Glu Lys  
 245 250 255  
 Arg Asn Gly Val Val Leu Leu Phe Ser Ala His Ser Leu Pro Met Ser  
 260 265 270  
 Val Val Asn Arg Gly Asp Pro Tyr Pro Ala Glu Val Ala Ala Thr Val  
 275 280 285  
 His Ala Val Met Gln Arg Leu Asn Phe Ser Asn Pro Tyr Arg Leu Cys  
 290 295 300  
 Trp Gln Ser Gln Val Gly Pro Ser Ala Trp Leu Gly Ala Gln Thr Ser  
 305 310 315 320  
 Asp Thr Val Glu Asn Tyr Val Lys Arg Gly Gln Thr Asp Ile Ile Leu  
 325 330 335  
 Val Pro Ile Ala Phe Thr Ser Asp His Ile Glu Thr Leu Tyr Glu Leu  
 340 345 350  
 Asp Leu Glu Val Ile Lys Glu Ala Asn Ser Pro Gly Val Lys Arg Ala  
 355 360 365  
 Glu Ser Leu Asn Gly Asn Pro Ile Phe Ile Gln Ala Leu Ala Asp Ile  
 370 375 380  
 Ala Gln Glu His Leu Arg Lys Gly Glu Lys Cys Ser Leu Gln Met Thr  
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<210> 52

<211> 1536

<212> DNA

<213> *Aspergillus fumigatus*

<400> 52

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 tatgggatgt acccgatctc ctctcttctc acacttgacc cttcaatgac tccctaccg 600

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&lt;210&gt; 53

&lt;211&gt; 1536

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;400&gt; 53

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&lt;210&gt; 54

&lt;211&gt; 512

&lt;212&gt; PRT

<213> *Aspergillus fumigatus*

&lt;400&gt; 54

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 35 40 45  
 Gly Ile Ala Asp His Glu Ser Thr Pro Ser Thr Val Gln Lys Thr Tyr  
 50 55 60  
 Phe Ser Ala Asn Arg Thr Ala Asp Gly Leu Leu Ala Ser Leu Ser Ala  
 65 70 75 80  
 Val Asn Ser Ser Pro Arg Ser Ile Ala Asp Asn Ala Leu Ser Gln Gly  
 85 90 95  
 Ala Ala Ser Ser Glu Ser Ile Thr Ser Gln Ser Thr Ser Gln Glu Leu  
 100 105 110  
 Pro His Arg Arg Arg Lys Arg Leu Lys Glu Glu Ala Ala Lys Asn Asn  
 115 120 125  
 Ala Ala Glu Thr Glu Leu Pro Pro Asp Ala Ser Ser Gln Leu Ser Thr  
 130 135 140  
 Leu Ser Ser Ala Leu Pro Ala Thr Ser Leu Arg Arg Lys Leu Ala Ala  
 145 150 155 160  
 Phe Leu Ala Leu Thr Lys Pro Arg Leu Ser Phe Leu Ile Val Leu Thr  
 165 170 175  
 Thr Thr Ser Ala Tyr Gly Met Tyr Pro Ile Ser Ser Leu Leu Thr Leu  
 180 185 190  
 Asp Pro Ser Met Thr Pro Leu Pro Thr Leu Ser Thr Ser Thr Leu Thr  
 195 200 205  
 Phe Leu Tyr Leu Thr Thr Gly Thr Phe Leu Ser Ser Cys Ser Ala Asn  
 210 215 220  
 Thr Leu Asn Met Leu Leu Glu Pro Lys Tyr Asp Ala Leu Met Ser Arg  
 225 230 235 240  
 Thr Arg Asn Arg Pro Leu Val Arg Gly Leu Leu Ser Arg Arg Ala Ala  
 245 250 255  
 Val Leu Phe Ala Ile Ala Thr Ala Ala Ala Gly Leu Gly Leu Leu Tyr  
 260 265 270  
 Ile Gly Thr Asn Pro Thr Thr Thr Ala Leu Ser Ala Ser Asn Ile Cys  
 275 280 285  
 Leu Tyr Ala Phe Val Tyr Thr Pro Leu Lys Arg Ile Ser Val Ile Asn  
 290 295 300  
 Thr Trp Val Gly Ala Val Val Gly Gly Ile Pro Pro Leu Met Gly Trp  
 305 310 315 320  
 Thr Ala Ala Ala Gly Gln Thr Ala Thr Thr Gly His Asp Ser Trp Arg  
 325 330 335  
 Asp Met Leu Phe Ser Lys Asp Ser Ile Gly Gly Trp Leu Leu Gly Gly

340	345	350
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355	360	365
Ile Arg Glu Glu Tyr Lys Ala Ala Gly Tyr Arg Met Leu Ala Trp Thr		
370	375	380
Asn Pro Ala Ala Asn Ala Arg Val Ala Leu Arg Tyr Ser Leu Leu Met		
385	390	395
Phe Pro Phe Ser Val Gly Leu Trp Trp Val Gly Val Val Gly Asn Gly		
405	410	415
Phe Leu Val Gly Ser Thr Ala Ala Asn Gly Trp Leu Val Lys Glu Ala		
420	425	430
Tyr Lys Phe Trp Arg His Gln Gly Ala Asn Gly Ser Ala Arg Arg Leu		
435	440	445
Phe Trp Ala Ser Ile Trp Gln Leu Pro Ile Leu Leu Val Gly Gly Leu		
450	455	460
Val Thr Lys Lys Gly Leu Trp Asp Gly Val Trp Asn Asn Val Phe Gly		
465	470	475
Gln Pro Val Glu Asp Glu Asp Asp Tyr Leu Trp Glu Asp Glu Asp Glu		
485	490	495
Val Ala Glu Ala Glu Arg Lys Met Ile Pro Ala Lys Thr Ser Ser Ser		
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&lt;210&gt; 55

&lt;211&gt; 1626

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;400&gt; 55

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<210> 56

<211> 1626

<212> DNA

<213> *Aspergillus fumigatus*

<400> 56

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<210> 57

<211> 542

<212> PRT

<213> *Aspergillus fumigatus*

<400> 57

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      20              25              30

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Ala Pro Leu Phe Ser Thr Ala Pro Phe Arg Arg Gln Leu His Ala Ser

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Thr	Leu	Glu	Ala	His	Arg	Ser	Ser	Asn	Arg	Ala	Ser	Leu	Ile	Arg	Lys	
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Val	Ile	Asn	His	Asp	Cys	Pro	Ala	Glu	Thr	Pro	Pro	Pro	Ile	Leu	Pro	
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Pro	Gln	Thr	Thr	Glu	Tyr	Pro	Gln	Leu	Gln	Trp	His	Ala	Asp	Glu	Thr	
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Trp	Lys	Thr	Pro	Asp	Ala	Val	Ser	Arg	Leu	Asp	Ala	Glu	Ile	Arg	Ala	
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 Tyr Gly Ser Asp Ile Asp Leu Thr Thr Thr Gly Val Ser Val Asp Pro  
 405 410 415  
 Pro Ser Trp Phe Asn Ala Ser Thr Val Lys Arg Ala Ser Ala Leu Tyr  
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 Ala Pro Asp Asp Leu Pro Ala His Leu Arg Gly Gln Arg Ser Leu Ile  
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 Ser Leu Lys Arg Thr Ala Ala Ala Arg Arg Asn Leu Pro Ala Ala Ser  
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 Arg Leu Cys Val Gln Asp Pro Thr Asn Tyr Met Asn Asp Leu Gly Arg  
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 Ser Cys Val Arg Thr Leu Glu Leu Gln His Thr Phe Ser Leu Ala His  
 485 490 495  
 Asp Arg Leu Gly Ala Ser Leu Lys Arg Trp Asp Asp Ser Glu Pro Ala  
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&lt;210&gt; 58

&lt;211&gt; 2356

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;400&gt; 58

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&lt;210&gt; 59

&lt;211&gt; 2356

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;400&gt; 59

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<211> 785

<212> PRT

<213> *Aspergillus fumigatus*

<400> 60

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```

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```

```

Leu Glu Ser Gly Leu Gly Arg Arg Asn Phe Val Pro Pro Arg Gln Val
      35          40          45

```

```

Pro Val Val Asp Ala Met Glu Arg Thr Lys Asn Ala Ile Gln Ser Asn
      50          55          60

```

```

Asn Ser Ser Ser Arg Ala Gln Leu Ser Asp Ala Leu Pro Glu Ser Glu
      65          70          75          80

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```

Lys Ser Gln Ser Ala Gly Gln Val Ile Val Pro Thr Arg Met Gln Glu
          85          90          95

```

```

Leu Leu Asp Arg Gly Arg Pro Ile Glu Ala Ala Gln Phe Phe Leu Glu
      100          105          110

```

```

Thr His Ala Ala Ser Leu Lys Gly Ile Ser Ser Asp Arg Lys Glu Met
      115          120          125

```

```

Ala Thr Lys Val Phe Phe Val Asn Cys Lys Glu Asp Asn Val Phe Ile
      130          135          140

```

```

Ala Arg Ser Val Phe Glu Arg Leu Glu Glu Val Asp Arg Ile Thr Pro
      145          150          155          160

```

```

Glu Met Trp Lys Thr Leu Met Leu Ala Leu Ala Lys Lys Gly Cys Ile
          165          170          175

```

```

Glu Ser Val Ala Ser Val Tyr Thr Arg Tyr Met Arg Lys Phe Pro Cys
      180          185          190

```

```

Pro Pro Glu Met Val Asp Val Val Leu Arg Ser Leu Leu Glu Ser His
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```

```

Arg Leu Thr Thr Ala Lys Trp Phe Leu Leu Arg Asn Leu Gln His Asp
      210          215          220

```

```

Arg Asp Cys Gly Leu Cys Gly Ala Tyr Leu Ser Gly Leu Trp Arg Lys
      225          230          235          240

```

Thr Arg Ser Ile Glu Leu Leu Asn Gly Gln Leu Lys Lys Ile Leu Thr  
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 Val Ile Lys Ala Tyr Val Glu Phe Gly Arg Val Ala Asp Ala Glu Ala  
 275 280 285  
 Leu Val His Asp Met Thr Thr Leu Tyr Gly Ile Pro Leu Arg Cys Arg  
 290 295 300  
 Thr Gln Gly Leu Leu Val Tyr Ala Lys Ala Leu Asn Cys Asp Trp Glu  
 305 310 315 320  
 Gly Val Asp Ala Gly Leu Gln Glu Met His Lys Leu Lys Leu Thr Arg  
 325 330 335  
 Arg Arg Arg Asp Phe Leu Pro Ile Phe Asp Arg Ile Phe Leu Glu Tyr  
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 Thr Ser Met Ala Lys Gln Arg Ser Trp Asn Ile Pro Ile Asn Glu Gln  
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 Pro Val Gly Phe Trp Gln Met Leu Gln Ala Ala Arg Val Lys Tyr Gly  
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 His Ser Ser Thr Ser Gln Arg Ile Met Gly Tyr Asp Gln Gln Ser Phe  
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 Pro Leu Pro Glu Val Asn Ser Met Pro Tyr Thr Gln Asn Pro Leu Ser  
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 485 490 495  
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 545 550 555 560  
 Arg Thr Ile Arg His Leu Val Arg Phe Ser Pro Ile Phe Phe Arg Gln

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Arg	Ala	Phe	Ala	Ala	Thr	Asp	Asn	Ile	Leu	Gly	Leu	Arg	Trp	Cys	Ile
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	675						680					685			
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Ile	Ala	Asp	Leu	Leu	Glu	Glu	Lys	Asn	Glu	Gly	Cys	Ala	Pro	Ile	Trp
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21

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<210> 76

<211> 20

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<213> Artificial sequence

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<223> PCR primer 2.1.1.1

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20

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<213> Artificial sequence

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<223> PCR primer 2.1.1.2

<400> 78

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20

<210> 79

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<223> PCR primer 2.1.1.6



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<223> PCR primer 2.1.1.9

<400> 81  
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<210> 82  
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<223> PCR primer 4.3.4.2

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<223> PCR primer 6.8.13.2

<400> 84  
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<210> 85  
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<223> PCR primer 7.5.9.3

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<210> 86  
<211> 20  
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<220>  
<223> PCR primer 7.5.9.4

<400> 86  
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<210> 87  
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<212> DNA  
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<220>  
<223> PCR primer 8.62.2

<400> 87  
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<210> 88  
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<220>  
<223> PCR primer Gt11f1

<400> 88  
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<210> 89  
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<220>  
<223> PCR primer Gt11f3

<400> 89  
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<210> 90  
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<220>  
<223> PCR primer Gt11Rev

<400> 90

ttgacaccag accaactggt aatg

24

<210> 91

<211> 3052

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA228; clone 8-47; contig 4842 region 234347-231296

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 91

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gtgcatcaaa tggcctgtat gcgaacatgg tccctgggta acggaagcca gtctgtttcc 2940
aagcgagggtc aattttcaacg gtgtcctctc tagtgggtgt cttcctgcaa ccaggcatgg 3000
tatgatttgt cggccttttag tgccatttcc tgagtcaagc aggacagggtc aa 3052

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<210> 92
<211> 2052
<212> DNA
<213> Aspergillus fumigatus

```

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<220>
<223> Phylum CEA228; clone 8-47; contig 4842 region 234347-231296
      Genomic sequence containing the coding region

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<210> 93
<211> 2052
<212> DNA
<213> Aspergillus fumigatus

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<220>
<223> Phylum CEA228; clone 8-47; contig 4842 region 234347-231296
      Coding region without exons

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&lt;400&gt; 93

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&lt;210&gt; 94

&lt;211&gt; 683

&lt;212&gt; PRT

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA228; clone 8-47; contig 4842 region 234347-231296  
Protein sequence

&lt;400&gt; 94

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Ser Ala Glu Ala Ala Ala Ser Asp Gly Gly Gln Asp Leu Thr Thr Ile
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Leu Asp Arg Ser Gln Arg Gly Glu Leu Thr Val Leu Val Ala Leu Ile
35          40          45

Ala Gln Arg Met Arg Asp Gly Ile Glu Gln Asn Phe Ser Asn Ala Pro
50          55          60

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 65 70 75 80  
 Leu Pro Gln Ser Thr Asp Ala Gln Glu Asp Gln Ser Ser Ser Gly Ser  
 85 90 95  
 Ala Ala Asn Gly Ser Arg Thr Asp Pro Gln Phe Lys Asp Pro Glu Thr  
 100 105 110  
 Ala Thr Cys Ala Leu Ser Lys Tyr Asp Asp Trp Arg Asp Ser Val Leu  
 115 120 125  
 Leu Arg Ile Gly Glu Val Val Asn Arg Asp Pro Glu His Gly Glu Val  
 130 135 140  
 Gln Ala Asn Glu Asn Pro Pro Ser Gly Gln Gln Ser Gln Gln Ile Arg  
 145 150 155 160  
 Ser Glu Glu Asp Asp Arg Ser Ile Arg Lys Leu Arg Glu Val Phe Pro  
 165 170 175  
 Pro Val Glu Thr Ser Leu Ser Gln Leu Pro Glu Ala Lys Lys Leu Leu  
 180 185 190  
 Ile Leu His Ser Leu Leu Leu Leu Val Leu Ser Leu Glu His Tyr Asn  
 195 200 205  
 Ala Trp Ser Arg Val Leu Met Leu Phe Val Thr Ser Ser Leu Gly Leu  
 210 215 220  
 Asp Val Lys Leu Leu Asn Glu Asp Glu Val Lys Val Ala Arg Gly Leu  
 225 230 235 240  
 Leu Asp Thr Ala Leu Ala Leu Ser Ser Asn Ala Pro Arg Gln Asp Glu  
 245 250 255  
 Ser Arg Ser Arg Asp Ser Ser Arg Lys Trp Lys Val Gly Ile Ala Ser  
 260 265 270  
 Val Ala Gly Ala Ala Leu Ile Gly Ile Thr Gly Gly Leu Ala Ala Pro  
 275 280 285  
 Leu Val Ala Ala Gly Leu Gly Thr Val Met Gly Gly Leu Gly Leu Gly  
 290 295 300  
 Ala Thr Ala Ala Ala Gly Tyr Leu Gly Ala Leu Ala Gly Ser Gly Val  
 305 310 315 320  
 Val Val Gly Gly Leu Phe Gly Ala Tyr Gly Gly Arg Met Thr Gly Arg  
 325 330 335  
 Met Val Asp Lys Tyr Ala Arg Glu Val Asp Asp Phe Ala Phe Leu Pro  
 340 345 350  
 Ile Arg Gly Ser Arg His Arg Ser Glu Asp Glu Arg Glu Ala Ala His  
 355 360 365  
 Gln Asp His Arg Leu Arg Val Thr Ile Gly Val Thr Gly Trp Leu Thr  
 370 375 380  
 Glu Glu Asp Asn Phe Val Ile Pro Trp Arg Val Ile Gly Ala Glu Ser

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	405		410			415
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	420		425			430
Gln Val Leu Lys Lys Thr Phe	Leu Ser Gln Leu Leu Thr	Ala Val Ala				
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Leu Pro Leu Gly Leu Leu Lys	Val Ala Arg Val Val Asp Asn Pro Phe					
	450		455			460
Ser Val Ala Lys Ala Arg Ala Asp Lys Ala Gly Glu Val Leu Ala Asp						
465		470		475		480
Ala Leu Ile Ser Lys Val Gln Gly Glu Arg Pro Val Thr Leu Ile Gly						
	485		490			495
Tyr Ser Leu Gly Ser Arg Val Ile Phe Ala Cys Leu Gln Ser Leu Ala						
	500		505			510
Lys Arg Arg Ala Phe Gly Leu Val Glu Ser Ala Ile Leu Met Gly Ala						
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Pro Thr Pro Ser Asn Ser Glu Gln Trp Cys Arg Ile Arg Ser Val Val						
	530		535			540
Ser Gly Arg Leu Val Asn Val Tyr Ser Glu Asn Asp Ser Val Leu Ala						
545		550		555		560
Leu Leu Tyr Arg Thr Ser Ser Leu Gln Leu Gly Val Ala Gly Leu Gln						
	565		570			575
Pro Val Glu Gly Val Ser Gly Val Glu Asn Leu Asp Val Ser Asp Leu						
	580		585			590
Ile Ser Gly His Leu Arg Tyr Gln Phe Leu Val Gly Arg Ile Leu Ser						
	595		600			605
Val Val Gly Leu Glu Ser Ile Asp Ala Arg Glu Val Ala Leu Glu Glu						
	610		615			620
Ala Ala Leu Glu Ala Lys Asp Arg Arg Gln Glu Gln Glu Arg Ala His						
625		630		635		640
Asn Glu Arg Gln Ala Gly Phe Met Gly Glu Gly Arg Ser Pro Ser Gln						
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Arg Leu Glu Ser Gln Glu Asp Leu Gln Gly Glu Glu Asp Arg Leu Gln						
	660		665			670
Lys Glu Met Gly Lys Ala Arg Val Arg His Ser						
	675		680			

&lt;210&gt; 95

&lt;211&gt; 3814

&lt;212&gt; DNA

&lt;213&gt; Aspergillus fumigatus

&lt;220&gt;

<223> Phylum CEA229; clone 8-62; contig 4938 region 215653-219466  
 Genomic sequence containing 3' and 5'-ends and the coding region

&lt;400&gt; 95

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gtgccatttg	tcgtccccca	acttttcttt	cgggcattgt	ccccattagt	tgagctttat	420
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&lt;210&gt; 96

&lt;211&gt; 2814

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA229; clone 8-62; contig 4938 region 215653-219466  
Genomic sequence containing the coding region

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&lt;210&gt; 97

&lt;211&gt; 2814

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA229; clone 8-62; contig 4938 region 215653-219466  
Coding region without exons

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<210> 98

<211> 937

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<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA229; clone 8-62; contig 4938 region 215653-219466  
Protein sequence

<400> 98

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50          55          60

Ala Pro Asn Tyr Asp Ala Thr Ser Ala Ala Lys Arg Leu Ala Arg Met
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Met Glu Ala Ala Glu Ala Gly Glu Phe Met Gly Leu Ala Ser Leu Lys
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Thr Arg Ser Gln Leu Val Asp Ala Leu Ile Ser Arg Pro Asn Leu Glu
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Ser Gly Leu Gly Arg Arg Asn Phe Val Pro Pro Arg Gln Val Pro Val
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Ser Ser Arg Ala Gln Leu Ser Asp Ala Leu Pro Glu Ser Glu Lys Ser
195         200         205

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<210> 99

<211> 2401

<212> DNA

<213> Aspergillus fumigatus

$\langle 220 \rangle$

<223> Phylum CEA230; clone 9-11; contig 4899 region 9642-7242

Genomic sequence containing 3' and 5'-ends and the coding region

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<210> 100
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<212> DNA
<213> Aspergillus fumigatus

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<220>
<223> Phylum CEA230; clone 9-11; contig 4899 region 9642-7242
      Genomic sequence containing the coding region

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<210> 101
<211> 1200
<212> DNA
<213> Aspergillus fumigatus

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<220>
<223> Phylum CEA230; clone 9-11; contig 4899 region 9642-7242
      Coding region without exons

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gccgttgggt tagaccgaa tcgctcaacg attttctacc agtccgccgt ccatgcacac 420
gccgaactat tttggatttt gtgcacaata gcctctatgg gatattcttc ccgaatgaca 480
cagtgaaga aggaacagct agctgacgtc ggccagagca aactccagtt gcctgataac 540
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<210> 102

<211> 399

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA230; clone 9-11; contig 4899 region 9642-7242  
Protein sequence

<400> 102

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Glu Val Phe Arg Arg Trp Ser Ser Ser Glu Thr Ala Lys Ser Ser Ser
35        40        45

Ala Ala Asn Gln Thr Ile Phe Ser Gly Ile Gln Pro Thr Gly Val Pro
50        55        60

His Leu Gly Asn Tyr Leu Gly Ala Leu Arg Glu Trp Val Arg Leu Gln
65        70        75        80

Asn Ala Ala Lys Glu Gly Thr Arg Leu Phe Phe Ser Ile Val Asp Leu
85        90        95

His Ala Leu Thr Val Pro Gln Asp Ala Ser Gln Leu Arg Asn Trp Arg
100       105       110

Lys Glu Thr Phe Ala Thr Leu Ile Ala Val Gly Leu Asp Pro Asn Arg
115       120       125

Ser Thr Ile Phe Tyr Gln Ser Ala Val His Ala His Ala Glu Leu Phe
130       135       140

Trp Ile Leu Cys Thr Ile Ala Ser Met Gly Tyr Leu Ser Arg Met Thr
145       150       155       160

Gln Trp Lys Lys Glu Gln Leu Ala Asp Val Gly Gln Ser Lys Leu Gln
165       170       175

Leu Pro Asp Asn Ala Asn Leu Glu Asp Ser Thr Ala Arg Ser Arg Leu
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Arg Leu Gly Leu Phe Ser Tyr Pro Val Leu Gln Ala Ala Asp Ile Leu
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Ile Arg Ala Thr His Val Pro Val Gly Asp Asp Gln Arg Gln His Leu  
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 Ile Phe Pro Ser Pro Glu Ala Ile Ile Ser Pro Ala Lys Arg Val Met  
 245 250 255  
 Ser Leu Lys Glu Pro Thr Leu Lys Met Ser Lys Ser His Ala Asp Arg  
 260 265 270  
 Arg Ser Arg Ile Ile Leu Thr Asp Ser Pro Ala Glu Ile Ser Lys Lys  
 275 280 285  
 Ile Asn Ala Ala Leu Thr Asp Ser Glu Leu Thr Ile Thr Tyr Asp Pro  
 290 295 300  
 Val Arg Arg Pro Gly Val Ala Asn Leu Ile Glu Ile Leu Ser His Phe  
 305 310 315 320  
 Asp Gly Arg Thr Cys Asp Glu Ile Ala Met Glu Tyr Arg Ser Ala Ser  
 325 330 335  
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 340 345 350  
 Glu Pro Ile Arg Glu Lys Tyr Leu Ser Leu Val Gly Asp Gln Thr Asp  
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 385 390 395

<210> 103

<211> 3805

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA231; clone 10-80; contig 4940 region 54154-50350  
 Genomic sequence containing 3' and 5'-ends and the coding region

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&lt;210&gt; 104

&lt;211&gt; 2805

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA231; clone 10-80; contig 4940 region 54154-50350  
 Genomic sequence containing the coding region

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 ccacgtggca agagcgagct gaagagtacg gacgatatcc ggattgcgcg caaattgaag 2760  
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<210> 105

<211> 2805

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA231; clone 10-80; contig 4940 region 54154-50350  
 Coding region without exons

<400> 105

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&lt;210&gt; 106

&lt;211&gt; 934

&lt;212&gt; PRT

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA231; clone 10-80; contig 4940 region 54154-50350  
Protein sequence

&lt;400&gt; 106

Met Pro His Arg Ala Ala Ser Pro Ala Val Ser Glu Asn Glu Phe Asp

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Ile Thr Gly Ala Leu Phe Gln Asn Asp Ser Asp Ser Asp Asn Glu Gln	20	25	30
Pro Ser Ala Lys Ser Lys Arg Gln Pro Pro Lys Lys Val Pro Ser Gln	35	40	45
Ala Leu Asp Phe Leu Gly Asp Val Asn Glu Asp Asp Asn Asp Asp Glu	50	55	60
Ala Phe Ile Ala Glu Gln Gln Thr Ser Ala Asn Arg Lys Ala Ser Asn	65	70	75
Leu Lys Gly Arg Thr Val Lys Lys Gly Gly Gly Phe Gln Ala Met Gly	85	90	95
Leu Ser Ala Asn Leu Leu Lys Ala Ile Ala Arg Lys Gly Phe Ser Val	100	105	110
Pro Thr Pro Ile Gln Arg Lys Thr Ile Pro Val Ile Met Asp Asp Gln	115	120	125
Asp Val Val Gly Met Ala Arg Thr Gly Ser Gly Lys Thr Ala Ala Phe	130	135	140
Val Ile Pro Met Ile Glu Lys Leu Lys Ser His Ser Thr Lys Val Gly	145	150	155
Ala Arg Gly Leu Val Leu Ser Pro Ser Arg Glu Leu Ala Leu Gln Thr	165	170	175
Leu Lys Val Val Lys Glu Leu Gly Arg Gly Thr Asp Leu Lys Ser Val	180	185	190
Leu Leu Val Gly Gly Asp Ser Leu Glu Glu Gln Phe Ala Met Ile Ala	195	200	205
Gly Asn Pro Asp Ile Ile Ile Ala Thr Pro Gly Arg Phe Leu His Leu	210	215	220
Lys Val Glu Met Asn Leu Asp Leu Ser Ser Ile Arg Tyr Val Val Phe	225	230	235
Asp Glu Ala Asp Arg Leu Phe Glu Met Gly Phe Ala Ala Gln Leu Thr	245	250	255
Glu Ile Leu His Gly Leu Pro Ala Asn Arg Gln Thr Leu Leu Phe Ser	260	265	270
Ala Thr Leu Pro Lys Ser Leu Val Glu Phe Ala Arg Ala Gly Leu Gln	275	280	285
Glu Pro Thr Leu Val Arg Leu Asp Thr Glu Ser Lys Ile Ser Pro Asp	290	295	300
Leu Gln Asn Ala Phe Phe Ser Val Lys Ser Ser Glu Lys Glu Gly Ala	305	310	315
Leu Leu Tyr Ile Leu His Glu Val Ile Lys Met Pro Thr Gly Pro Thr	325	330	335

Glu Val Ser Gln Gln Arg Lys Glu Glu Asp Ala Ser Ala Lys Asn Leu  
 340 345 350  
 Lys Asn Lys Lys Arg Lys Arg Ala Glu Met Glu Lys Ala Val Asn Thr  
 355 360 365  
 Arg Glu Ser Pro Thr Lys His Ser Thr Ile Val Phe Ala Ala Thr Lys  
 370 375 380  
 His His Val Asp Tyr Leu Tyr Ser Leu Leu Cys Glu Ala Gly Phe Ala  
 385 390 395 400  
 Val Ser Tyr Val Tyr Gly Ser Leu Asp Gln Thr Ala Arg Lys Ile Gln  
 405 410 415  
 Val Gln Asn Phe Arg Thr Gly Met Thr Asn Ile Leu Val Val Thr Asp  
 420 425 430  
 Val Ala Ala Arg Gly Ile Asp Ile Pro Ile Leu Ala Asn Val Ile Asn  
 435 440 445  
 Tyr Asp Phe Pro Ser Gln Pro Lys Ile Phe Val His Arg Val Gly Arg  
 450 455 460  
 Thr Ala Arg Ala Gly Arg Lys Gly Trp Ser Tyr Ser Leu Val Arg Asp  
 465 470 475 480  
 Ala Asp Ala Pro Tyr Leu Leu Asp Leu Gln Leu Phe Leu Gly Arg Arg  
 485 490 495  
 Leu Val Val Gly Arg Glu Phe Gly Asp Gln Val Asn Phe Ala Glu Asp  
 500 505 510  
 Val Val Thr Gly Ser Leu Pro Arg Asp Gly Leu Ser Gln Ser Cys Glu  
 515 520 525  
 Trp Val Thr Lys Val Leu Asp Asp Asn Ala Asp Leu Ala Ala Gln Arg  
 530 535 540  
 Thr Val Ala Ala Lys Gly Glu Lys Leu Tyr Met Arg Thr Arg Asn Ala  
 545 550 555 560  
 Ala Ser Leu Glu Ser Ala Lys Arg Ser Lys Gln Val Val Ser Ser Asp  
 565 570 575  
 Asn Trp Thr Ser Val His Pro Leu Phe Gln Asp Glu Thr Ser Asn Leu  
 580 585 590  
 Glu Ala Glu Arg Glu Lys Met Leu Ala Arg Ile Gly Gly Tyr Arg Pro  
 595 600 605  
 Pro Glu Thr Ile Phe Glu Val Asn Asn Arg Arg Met Gly Lys His Glu  
 610 615 620  
 Asn Val Asp Ala Leu Asp Thr Ile Lys Arg Val Arg Ser Thr Leu Glu  
 625 630 635 640  
 Ser Lys Lys Lys Arg Ala Gln Ala Asn Glu Lys Ser Glu Phe Leu Glu  
 645 650 655

Asp Gly Pro Asp Asp Gly Lys Ala Val Asn Glu Ala Lys Glu Thr Glu  
 660 665 670  
 Ser Glu Gly Ala Phe Ser Asp Glu Asp Asp Asp Val Pro Thr Gly Val  
 675 680 685  
 Ala Asp Asn Met Ser Met Ala Ser Asp Ser Glu Leu Glu Val Thr Phe  
 690 695 700  
 Ser Ser Tyr Ser Lys Ser Lys Asp Asn Lys Ala Lys Lys Ala Ser Ala  
 705 710 715 720  
 Ala Ser Phe Gln Asn Pro Glu Tyr Phe Met Ser Tyr Thr Pro Asn Asn  
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 Thr Ser Leu Ala Glu Asp Arg Ala Tyr Gly Val His Ser Gly Thr Asn  
 740 745 750  
 Ser Asn Phe Ala Gln Ala Ser Arg Ser Ala Thr Met Asp Leu Ala Gly  
 755 760 765  
 Asp Asp Gly Gly Arg Gly Phe Gly Glu Ala Arg Thr Leu Met Arg Trp  
 770 775 780  
 Asp Lys Arg His Lys Lys Tyr Val Ala Arg Gln Asn Asp Glu Asp Gly  
 785 790 795 800  
 Ser Lys Gly Thr Arg Leu Val Arg Gly Glu Ser Gly Ala Lys Ile Ala  
 805 810 815  
 Ala Ser Phe Arg Ser Gly Arg Phe Asp Ala Trp Lys Arg Glu Asn Arg  
 820 825 830  
 Leu Gly Arg Leu Pro Arg Val Gly Glu Ala Glu Ala Ala Asn Leu Ala  
 835 840 845  
 Ala Gly Leu Asn Ala Ala Ile Ser Gly Lys Arg Phe Arg His Arg Lys  
 850 855 860  
 Glu Gln Ala Pro Lys Lys Ala Asp Pro Leu Arg Gly Asp Tyr Glu Lys  
 865 870 875 880  
 Met Lys Lys Lys Ala Glu Leu Ala Lys Glu Arg Ala Met Ser Lys Ala  
 885 890 895  
 Gly Gly Ala Ala Pro Arg Gly Lys Ser Glu Leu Lys Ser Thr Asp Asp  
 900 905 910  
 Ile Arg Ile Ala Arg Lys Leu Lys Gln Lys Arg Arg Glu Lys Asn Ala  
 915 920 925  
 Arg Pro Ser Arg Lys Lys  
 930

&lt;210&gt; 107

&lt;211&gt; 2413

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA232; clone 10-175; contig 4938 region 211008-213420  
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 107

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tgctgcctgc	gtgcccaccg	acttcaccag	tgacgcgata	tcgtcatcgg	agcaacgcgg	240
gggaaacacg	aacatcacgt	gaatgcgcca	agacttgatg	accccaaatt	attactgatt	300
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ttacagatcc	ttcgtgccac	gattctttca	ttgagtggtc	aaatactact	cgacgtattt	420
ttgtgggctt	cagtttgttg	ctaattgttag	accgatagac	gacggccaac	ctttttaata	480
cactatcatic	gcacctcccc	atggctctcc	gccggccatt	aacacttccg	aggcacattc	540
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tggaacagaa	gaaattcttt	gctggcgacc	gattttcttc	tcttgtagtt	tagtgtattt	1920
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<210> 108

<211> 1413

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA232; clone 10-175; contig 4938 region 211008-213420  
Genomic sequence containing the coding region

<400> 108

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tcggccctct	cacgctcaag	cgcagaaccc	caaagatcca	acggcaatac	tcggatattg	420
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&lt;210&gt; 109

&lt;211&gt; 1287

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

&lt;223&gt; Phylum CEA232; clone 10-175; contig 4938 region 211008-213420

Coding region without exons

&lt;400&gt; 109

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gtcttctctca	acatgggtgg	gccatcgaag	attgacgaag	tggaagattt	tctgagcaga	240
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gatacggctg	aaaactatgt	caaacgtgga	cagaccgata	ttattctagt	tcccattgcc	1020
ttcaccagcg	accatattga	gactctgtac	gagttggatc	tggaagtgat	aaaggaagca	1080
aactccccgg	gagtcaagag	agccgagagt	ttgaatggta	accccathtt	cattcaggca	1140
ttagcagaca	ttgcccaaga	gcacctccgt	aagggagaga	agtgtcact	acagatgact	1200
ctgcgctgtc	aaggctgtaa	gagcgaacgg	tgcttggaa	agaagaaatt	ctttgctggc	1260
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&lt;210&gt; 110

&lt;211&gt; 428

&lt;212&gt; PRT

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA232; clone 10-175; contig 4938 region 211008-213420  
Protein sequence

&lt;400&gt; 110

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1           5           10           15

Ala Cys Leu Gly Leu Arg Pro Ala Val Ser Arg Ala Ala Leu Ala Tyr
          20           25           30

Gly Gln Glu Gln Arg Lys Gly Leu Ala Thr Ala Val Pro Pro Val Thr
          35           40           45

Gln Asn Ala Ala Gly Ser Lys Gly Pro Thr Ala Met Val Phe Leu Asn
          50           55           60

Met Gly Gly Pro Ser Lys Ile Asp Glu Val Glu Asp Phe Leu Ser Arg
65           70           75           80

Leu Phe Ala Asp Gly Asp Leu Ile Pro Leu Gly Arg Leu Gln Ser Tyr
          85           90           95

Leu Gly Pro Leu Ile Ala Lys Arg Arg Thr Pro Lys Ile Gln Arg Gln
          100          105          110

Tyr Ser Asp Ile Gly Gly Gly Ser Pro Ile Arg Lys Trp Ser Glu Tyr
          115          120          125

Gln Cys Glu Glu Met Cys Arg Leu Leu Asp Lys Ile Asn Pro Glu Thr
          130          135          140

Ala Pro His Lys Pro Tyr Val Ala Phe Arg Tyr Ala Asp Pro Leu Thr
145          150          155          160

Glu Glu Met Tyr Thr Lys Leu Leu Glu Asp Gly Phe Gly Asn Gly Lys
          165          170          175

Gly Gly Arg Ala Val Ala Phe Thr Gln Tyr Pro Gln Tyr Ser Cys Ser
          180          185          190

Thr Thr Gly Ser Ser Leu Asn Glu Leu Trp Lys Trp Arg Thr Arg Leu
          195          200          205

Glu Gly Lys Arg Ala Asn Gly Asn Met Asp Pro Ala Gly Ala Ile Gln
          210          215          220

Trp Ser Val Ile Asp Arg Trp Pro Thr His Pro Gly Leu Val Glu Ala
225          230          235          240

Phe Ala Arg Asn Ile Glu Glu Gln Leu Lys Thr Tyr Pro Glu Glu Lys
          245          250          255

Arg Asn Gly Val Val Leu Leu Phe Ser Ala His Ser Leu Pro Met Ser
          260          265          270

Val Val Asn Arg Gly Asp Pro Tyr Pro Ala Glu Val Ala Ala Thr Val
          275          280          285

His Ala Val Met Gln Arg Leu Asn Phe Ser Asn Pro Tyr Arg Leu Cys
          290          295          300

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Trp Gln Ser Gln Val Gly Pro Ser Ala Trp Leu Gly Ala Gln Thr Ser  
 305 310 315 320  
 Asp Thr Val Glu Asn Tyr Val Lys Arg Gly Gln Thr Asp Ile Ile Leu  
 325 330 335  
 Val Pro Ile Ala Phe Thr Ser Asp His Ile Glu Thr Leu Tyr Glu Leu  
 340 345 350  
 Asp Leu Glu Val Ile Lys Glu Ala Asn Ser Pro Gly Val Lys Arg Ala  
 355 360 365  
 Glu Ser Leu Asn Gly Asn Pro Ile Phe Ile Gln Ala Leu Ala Asp Ile  
 370 375 380  
 Ala Gln Glu His Leu Arg Lys Gly Glu Lys Cys Ser Leu Gln Met Thr  
 385 390 395 400  
 Leu Arg Cys Gln Gly Cys Lys Ser Glu Arg Cys Leu Glu Gln Lys Lys  
 405 410 415  
 Phe Phe Ala Gly Asp Arg Phe Ser Ser Leu Val Val  
 420 425

<210> 111

<211> 2865

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA233; clone 10-290; contig 4865 region 3495-6359

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 111

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acaaggcggg	atcgtctttc	aacacgcggg	cggtgagctt	atcagcgccg	attgcggggg	180
ggtgcagcaa	atcaagtcag	tcgccacttt	cggcgaccat	gacaaagcgc	aagattgggt	240
ttactaaacc	gcctactttt	tttttatcaa	agagacttgg	gtttgtcagc	ttttctttat	300
cttctgaaag	agcgctttct	tggtcaagct	gttcacaaaa	tccccatcac	tactgttccc	360
tttgtcggtta	ttttcgtcgc	attgcatcta	caacaaagaa	aacgggctcg	acgaaccctg	420
cgagatccat	acttctctggg	gtggcggtct	tcttagtcct	tatcgcatag	cggggtgctc	480
gaccagaagt	ccctgccacg	atgagtgcaa	tcctttctgc	agacgatttg	aacgatttca	540
tttctcccgg	ggttgcttgc	atcaagcccc	ttgagagtct	accacaaaaa	gaatcccagt	600
cggagggtatc	tttcctgtct	taccagtcac	ctggtgatat	cagccaatag	gctaacgctc	660
atttccaatt	caatagaatc	cctatgaggt	gacaaaggaa	gacaaagttc	aaccggaaaa	720
ccttcccccg	gtcagatatt	cattgactga	ttgccttgca	tgctccggat	gtgtcacgtc	780
tgcggaagca	gtgttgatat	ccttgcaatc	acatacggag	gttctcaata	ctcttgattc	840
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agcagacagc	gatggtcgca	tctttgttgc	tagcgtcagc	cctcaagtca	gggcgagctt	960
ggcagccaca	tacggaatca	ccgagcggga	ggcgaaatat	atgattgacc	aatttcttat	1020
gggcctcac	ggtctcagag	ctggtggaaa	acatggcaat	gggtttacat	gggttggtgga	1080
cacgaacgtt	atgcgtgaag	cagtgttggc	tctgacagcg	gacgaggtca	cgagctcttt	1140
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ctggatatgt	tatgctgaaa	aaacacaccc	ttttatcctt	ccgcatttat	ctgcctcaa	1260
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gctagcccgg	gtagatgaag	cgtactactc	tgcggactcg	gatagcgagg	gatctgtcac	2160
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atcgggatga	caaagcagcc	tagagcattt	ggcagaaaaa	gtgctctacc	ccaagtctga	2820
attctctcca	acaactcgcc	ttcaatcacc	cacgccccag	tttat		2865

&lt;210&gt; 112

&lt;211&gt; 1865

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA233; clone 10-290; contig 4865 region 3495-6359  
 Genomic sequence containing the coding region

&lt;400&gt; 112

atgagtgc	tcctttctgc	agacgatttg	aacgatttca	tttctcccgg	ggttgcttgc	60
atcaagcccc	ttgagagtct	accacaaaaa	gaatcccagt	cggaggtatc	tttctgtct	120
taccagtcat	ctgttgatat	cagccaatag	gctaacgctc	atttccaatt	caatagaatc	180
cctatgaggt	gacaaaggaa	gacaaagttc	aaccggaaaa	ccttcccccg	gctcagattt	240
cattgactga	ttgccttgca	tgtccggat	gtgtcacgtc	tgcggaagca	gtgttgatat	300
ccttgcaatc	acatacggag	gttctcaata	ctcttgattc	gtaccccgaa	ttgccgcttg	360
gttctacaag	ctaccaaaaga	ggcacacaaa	aagttggatc	agcagacagc	gatggctcgca	420
tctttgttgc	tagcgtcagc	cctcaagtca	ggcgagctt	ggcagccaca	tacggaatca	480
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cagtgttggc	tctgacagcg	gacgaggtca	cgagctcttt	attatcaact	ggatcgggca	660
gccttcccaa	gagtccaatt	ctttcgtccg	cttgccccgg	ctggatatgt	tatgctgaaa	720
aaacacaccc	ttttatcctt	cgcattttat	ctcgcctcaa	gtctcctcag	gcgttgagcg	780
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gtgtcataac	caccggtgag	ctactaactt	tagccactgc	tagggggctt	tctctaccca	1020
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caaatcgacg	acagcccatg	tcaaggaacg	cagctccggc	tggaaacaggc	gctgattatg	1440
catatgttga	agtcattggc	tgtcctggcg	gctgtaccaa	tggtggtggg	caaataagga	1500
ttgaagatgc	ccgggaggct	gttccgaacg	cactaaaaga	gacatcgact	gaaactcctg	1560

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tggctgcacc gaaacccacg ccgcatgagc agcgtgcctg gctagcccgg gtagatgaag 1620
cgtactactc tgcggactcg gatagcgagg gatctgtcac gacggagccg gtttctgtcc 1680
tgtcaaggga taaccagatt catgagtttt tgaactattg gtcagagaag gttgatatac 1740
ccctttcccg gctcgcgtac acgtcctatc gcgaagtggg gagcgacgtg ggtaagacga 1800
agaatgcgcc caacgaaact gctcgtgttg tggaattggc aggaaagatc ggaggtggtt 1860
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<210> 113
<211> 1725
<212> DNA
<213> Aspergillus fumigatus

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<220>
<223> Phylum CEA233; clone 10-290; contig 4865 region 3495-6359
Coding region without exons

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<400> 113
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acaaaggaag acaaagttca accggaaaac cttcccccg gctcagatttc attgactgat 180
tgctttgcat gctccggatg tgtcacgtct gcggaagcag tggtgatatc cttgcaatca 240
catacggagg ttctcaatac tcttgattcc gatggtcgca tctttgttgc tagcgtcagc 300
cctcaagtca gggcgagctt ggcagccaca tacggaatca ccgagcggga ggcgaaatat 360
atgattgacc aattttcttat gggccctcac ggtctcagag ctggtggaaa acatggcaat 420
gggtttacat gggttggtga cacgaacggt atgcgtgaag cagtgttggc tctgacagcg 480
gacgaggtca cgagctcttt attatcaact ggatcgggca gccttcccaa gagtccaatt 540
ctttcgctccg cttgccccgg ctggatatgt tatgctgaaa aaacacaccc ttttatcctt 600
ccgcatttat ctgcctcaa gtctcctcag gcgttgagcg gcacatttct gaagtcagtg 660
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cccgcgtcat gtttaactcc atttccagat caagccctag aatcattttt gttctctaag 960
agctcgtcgg gccaaacagt cgaatcaggg acatctggag gctatcttca tcacgtcctc 1020
caaactcttc aagccagaaa ccccggcagc aagattgtca cccagcgtgg gcgcaacgcc 1080
gatgttggtg aatatgtgct catgtcgtct ggggatgagc ctcttttttag ggcggctcgg 1140
tattatggct tcaggaatat acaaaatctc gtcagaaaac ttaaaccgcg acgcgtgtca 1200
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tgtcctggcg gctgtaccaa tgggtgggtgg caaataagga ttgaagatgc ccgggagggt 1380
gttccgaacg cactaaaaga gacatcgact gaaactcctg tggctgcacc gaaacccacg 1440
ccgcatgagc agcgtgcctg gctagcccgg gtagatgaag cgtactactc tgcggactcg 1500
gatagcgagg gatctgtcac gacggagccg gtttctgtcc tgtcaaggga taaccagatt 1560
catgagtttt tgaactattg gtcagagaag gttgatatac ccctttcccg gctcgcgtac 1620
acgtcctatc gcgaagtggg gagcgacgtg ggtaagacga agaatgcgcc caacgaaact 1680
gctcgtgttg tggaattggc aggaaagatc ggaggtggtt ggtga 1725

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<210> 114
<211> 574
<212> PRT
<213> Aspergillus fumigatus

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<220>
<223> Phylum CEA233; clone 10-290; contig 4865 region 3495-6359
Protein sequence

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<400> 114

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Met Ser Ala Ile Leu Ser Ala Asp Asp Leu Asn Asp Phe Ile Ser Pro

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1	5	10	15
Gly Val Ala Cys Ile Lys Pro Val Glu Ser Leu Pro Gln Lys Glu Ser	20	25	30
Gln Ser Glu Asn Pro Tyr Glu Val Thr Lys Glu Asp Lys Val Gln Pro	35	40	45
Glu Asn Leu Pro Pro Ala Gln Ile Ser Leu Thr Asp Cys Leu Ala Cys	50	55	60
Ser Gly Cys Val Thr Ser Ala Glu Ala Val Leu Ile Ser Leu Gln Ser	65	70	75
His Thr Glu Val Leu Asn Thr Leu Asp Ser Asp Gly Arg Ile Phe Val	85	90	95
Ala Ser Val Ser Pro Gln Val Arg Ala Ser Leu Ala Ala Thr Tyr Gly	100	105	110
Ile Thr Glu Arg Glu Ala Lys Tyr Met Ile Asp Gln Phe Leu Met Gly	115	120	125
Pro His Gly Leu Arg Ala Gly Gly Lys His Gly Asn Gly Phe Thr Trp	130	135	140
Val Val Asp Thr Asn Val Met Arg Glu Ala Val Leu Ala Leu Thr Ala	145	150	155
Asp Glu Val Thr Ser Ser Leu Leu Ser Thr Gly Ser Gly Ser Leu Pro	165	170	175
Lys Ser Pro Ile Leu Ser Ser Ala Cys Pro Gly Trp Ile Cys Tyr Ala	180	185	190
Glu Lys Thr His Pro Phe Ile Leu Pro His Leu Ser Arg Leu Lys Ser	195	200	205
Pro Gln Ala Leu Ser Gly Thr Phe Leu Lys Ser Val Leu Ser Lys Ala	210	215	220
Leu Gly Val Pro Pro Ser Gln Ile Trp His Leu Ala Ile Met Pro Cys	225	230	235
Phe Asp Lys Lys Leu Glu Ala Ser Arg Glu Glu Leu Thr Asp Ile Ala	245	250	255
Trp Ala Ser Thr Phe Thr Gln Ser Gln Thr Thr Pro Val Arg Asp Val	260	265	270
Asp Cys Val Ile Thr Thr Arg Glu Leu Leu Thr Leu Ala Thr Ala Arg	275	280	285
Gly Leu Ser Leu Pro Asn Leu Pro Leu Lys Pro Leu Pro Ala Ser Cys	290	295	300
Leu Thr Pro Phe Pro Asp Gln Ala Leu Glu Ser Phe Leu Phe Ser Lys	305	310	315
Ser Ser Ser Gly Gln Thr Val Glu Ser Gly Thr Ser Gly Gly Tyr Leu	325	330	335

His His Val Leu Gln Ile Phe Gln Ala Arg Asn Pro Gly Ser Lys Ile  
 340 345 350  
 Val Thr Gln Arg Gly Arg Asn Ala Asp Val Val Glu Tyr Val Leu Met  
 355 360 365  
 Ser Ser Gly Asp Glu Pro Leu Phe Arg Ala Ala Arg Tyr Tyr Gly Phe  
 370 375 380  
 Arg Asn Ile Gln Asn Leu Val Arg Lys Leu Lys Pro Ala Arg Val Ser  
 385 390 395 400  
 Arg Leu Pro Gly Ala Lys Pro Gln Ala Val Ser Ser Ser Ala Asn Arg  
 405 410 415  
 Arg Gln Pro Met Ser Arg Asn Ala Ala Pro Ala Gly Thr Gly Ala Asp  
 420 425 430  
 Tyr Ala Tyr Val Glu Val Met Ala Cys Pro Gly Gly Cys Thr Asn Gly  
 435 440 445  
 Gly Gly Gln Ile Arg Ile Glu Asp Ala Arg Glu Ala Val Pro Asn Ala  
 450 455 460  
 Leu Lys Glu Thr Ser Thr Glu Thr Pro Val Ala Ala Pro Lys Pro Thr  
 465 470 475 480  
 Pro His Glu Gln Arg Ala Trp Leu Ala Arg Val Asp Glu Ala Tyr Tyr  
 485 490 495  
 Ser Ala Asp Ser Asp Ser Glu Gly Ser Val Thr Thr Glu Pro Val Ser  
 500 505 510  
 Val Leu Ser Arg Asp Asn Gln Ile His Glu Phe Leu Asn Tyr Trp Ser  
 515 520 525  
 Glu Lys Val Asp Ile Pro Leu Ser Arg Leu Ala Tyr Thr Ser Tyr Arg  
 530 535 540  
 Glu Val Glu Ser Asp Val Gly Lys Thr Lys Asn Ala Pro Asn Glu Thr  
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 Ala Arg Val Val Glu Leu Ala Gly Lys Ile Gly Gly Gly Trp  
 565 570

<210> 115

<211> 1510

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA234; clone 10-304; contig 4899 region 443110-444619  
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 115

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cattttgtcc tgaagaagt aacaaaaagg ccaactcaga ctctttgcaa atgcaaggaa	120
gaggtaatga gaatgttttg ggagaagctt aaatgtagct ttgccggaac ggagaattga	180
gtaaagccgg tcatgaggcg ccaagacccc agcgaaaaag cagccctagg ccgcacgcaa	240

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ccccgttcgg cgagttgcta ctggctgtta agcgagactc ttgtgggcga agaccgcaac 300
acccgaaatt cgcgatccag tagcccagag cgacttgtgt gcgtttcgga cgactttgac 360
aatcccgaact cttcgacaac aaattcccat caccgccctc ccggagtctg tcgaccgtga 420
gtttgaaacc tacgccctat cgaatttctg gactgtcact gaagaatccg tttttgtcgt 480
tttttttagga agccttcgcc atggccgata tcgatgtcaa ggttgctcaa tggaagcttg 540
ttgaggttgg ccgtgttgtg ctgatccgca gcggtcctta caccggcaag cttgctgcca 600
ttgtcgagat catcgaccac aagcgtgtac gtttttcaac ggagaaattc tgagcgcagg 660
acggaaagat catggtcgga tgtgatattg acaaagaggc gcgatcatag gtcctggttg 720
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gactcaagaa gcaggtacgt tcagtttgcg aaactatggg agaattgtga tggcacattg 1020
gagggcattc ttggcaactc tgcactcgct tttcgcgaga gggaagagga gcaattactt 1080
gtattatgat ttgcgactgg ttactgacat ctggtgattt aacaggctcg ctacgaggtc 1140
cagaaggctc acgccaaggt cagggctgct gctcctaagt catagatgtt ttcagaggc 1200
tcggtgcata gtatgaaggg gtaccttggg acggttttac atggctgagg gttttattct 1260
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ggctctgggt tatagccgtc tccttagaca ttaattggga attaaacatt ttagactcaa 1440
gatcacgga tatgtaagaa agtatcgta tgtacattac tgagttggat tggctcgta 1500
tgactcgat 1510

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<210> 116

<211> 685

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA234; clone 10-304; contig 4899 region 443110-444619  
Genomic sequence containing the coding region

<400> 116

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ctgatccgca gcggtcctta caccggcaag cttgctgcca ttgtcgagat catcgaccac 120
aagcgtgtac gtttttcaac ggagaaattc tgagcgcagg acggaaagat catggtcgga 180
tgtgatattg acaaagaggc gcgatcatag gtcttggttg acggtccttc caccgaggag 240
aacaagatcg ttccccgtca cgctcttcct ctcgctcacg ccactctcac ccccttcgtc 300
attcccaaac tccccgcgc tgcgggcaact ggccccgtca agaagctctg ggagaagaac 360
gagatcgatg gaaagtgggc taagagcacc attgctcaga agactgagcg cgctgagcgg 420
aggaagaacc ttaccgactt cgagcgcttc aaggtcctca gactcaagaa gcaggtacgt 480
tcagtttgcg aaactatggg agaattgtga tggcacattg gagggcattc ttggcaactc 540
tgcactcgct tttcgcgaga gggaagagga gcaattactt gtattatgat ttgcgactgg 600
ttactgacat ctggtgattt aacaggctcg ctacgaggtc cagaaggctc acgccaaggt 660
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<210> 117

<211> 465

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA234; clone 10-304; contig 4899 region 443110-444619  
Coding region without exons

<400> 117

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aagcgtgtcc tgggtgacgg tccttccacc gaggagaaca agatcgttcc ccgtcacgct 180
cttctctctg ctcacgccac tctaccccc ttcgtcattc ccaaactccc ccgcgctgcc 240

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```

ggcactggcc ccgtaagaa gctctgggag aagaacgaga tcgatggaaa gtgggctaag   300
agcaccattg ctcagaagac tgagcgcgct gagcggagga agaacccttac cgacttcgag   360
cgcttcaagg tcctcagact caagaagcag gtcgctacg aggtccagaa ggctcacgcc   420
aaggtcaggg ctgctgctcc taagtcatag atgttttcat gaggc                     465

```

<210> 118

<211> 149

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA234; clone 10-304; contig 4899 region 443110-444619  
Protein sequence

<400> 118

```

Met Ala Asp Ile Asp Val Lys Val Ala Gln Trp Lys Leu Val Glu Val
1           5           10           15

```

```

Gly Arg Val Val Leu Ile Arg Ser Gly Pro Tyr Thr Gly Lys Leu Ala
          20           25           30

```

```

Ala Ile Val Glu Ile Ile Asp His Lys Arg Val Leu Val Asp Gly Pro
          35           40           45

```

```

Ser Thr Glu Glu Asn Lys Ile Val Pro Arg His Ala Leu Pro Leu Ala
          50           55           60

```

```

His Ala Thr Leu Thr Pro Phe Val Ile Pro Lys Leu Pro Arg Ala Ala
          65           70           75           80

```

```

Gly Thr Gly Pro Val Lys Lys Leu Trp Glu Lys Asn Glu Ile Asp Gly
          85           90           95

```

```

Lys Trp Ala Lys Ser Thr Ile Ala Gln Lys Thr Glu Arg Ala Glu Arg
          100          105          110

```

```

Arg Lys Asn Leu Thr Asp Phe Glu Arg Phe Lys Val Leu Arg Leu Lys
          115          120          125

```

```

Lys Gln Ala Arg Tyr Glu Val Gln Lys Ala His Ala Lys Val Arg Ala
          130          135          140

```

```

Ala Ala Pro Lys Ser
145

```

<210> 119

<211> 1942

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA254; clone 7-1-10; contig 4911 region 43163-41221  
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 119

```

tacaccagc acacctacc tagccacaga tttcttggac cacgggaacc cgaacaaaga   60
gtctctggcc gaactctggt ctaatttcct agagcaggag tcacaggcca gtgggaatcc   120
agaatcgccg aaaccatgaa gagtttcaaa aggtggctct gttctgagcc gtatagaaaa   180
ctagcatctt ctctaagata cggtggttcc acatttatat atgcttgccg actggctttg   240

```

gtctcctctt	cttttccatt	ctagacttgc	ttcgtagtaa	taacactgat	atcacccgcg	300
tgtttgcgac	ttttgcatca	aaccagcttc	cccacgcgtt	tctttctgcc	accatagcgg	360
gggacctcgt	tattgagcgg	acaagtcgtc	gttggtttt	tctgcacgtt	tggcctatgc	420
ttcgttttatt	cagctctggt	acagctggga	agttgactga	tacactctcc	tctctgattt	480
cttggtactc	cagattgaca	atgactaccg	gggctggtac	gatctctcat	tccaacacct	540
atcatcgat	tcctcgccgt	taactgacca	atccaccagt	gcaaagggtt	cgtccagtgg	600
tggatcggg	tccctctggg	actgggaagt	cgaccttgct	caagagactc	ttcgctgaat	660
accccgatac	tttcgattta	tccgtgtctc	gtacgtctaa	ccccttgcca	accctcattg	720
actatgcctg	cgaattgttt	cttttggtgg	aattgcgctg	aacggtgttt	gttatattta	780
gataccactc	gagctccccg	tcccggggaa	gaaaatggac	gtgagtatta	cttcacaact	840
aaagaagatt	tcctggatct	tgtgagcaag	aatgccttta	tcgagcatgc	gcagtttggg	900
ggcaattact	acggtactac	tgtgcaggca	gtgaaggatg	ttgcgcagaa	gggcaagatc	960
tgcgttctcg	acattgagat	gaggtaataa	tagtcctgca	acgtgaactg	atatgaccgg	1020
agaagcagag	gaaatccatc	atcaaattgga	ttgtagtcca	acccaaacaa	cagctgacga	1080
ctgaattgca	atagggcggtg	aaacaagtca	agcgcaccga	tcttgatgct	cgattcttat	1140
ttttagcacc	cccgtccctt	gaagaactag	agaaaagact	gcgtgggaga	gcaaccgaga	1200
ctgaggagag	cttgacggta	tggctgtcct	ccacattcct	tcacttcccc	aactcgccag	1260
actgtccccg	tgggaattcta	actttgcgtc	agaaacgcct	tgcccaagct	aaaaatgaat	1320
tggaaatatg	ggcgcagcct	ggctctcatg	ataagattgt	cgtgaacgat	gacctggaga	1380
aggcttataa	ggaactgcgg	gattggattg	tcgacggtgg	taactttgga	gcgcgtcaat	1440
gatttatttg	gcatgtctcg	gcgtgtttta	tttatcagcg	ctgctgtata	ctttagcgcc	1500
cgtagatact	gtcggttgcg	atactgaaaa	caatgcatac	tctgccttgg	taacttcggt	1560
ccacagaaac	ccataatcaa	ggaggtcctt	tcgtcgtcga	cgaacataag	agagattaat	1620
tacatgaaca	tcaagactat	gctaacaatt	cgaatgttgg	tctcttttct	gtctggagac	1680
gacaaatcta	ggaaagggtg	tagactcagt	cactctcttg	aacggagagg	agaaaattaa	1740
gcaaaactaa	aaaagagaac	aaagtctgat	gagcaatatg	agggtgaaa	aggatatctg	1800
taaagaggct	gctagaataa	aatggaagat	gccgattgag	aaggcaatgg	aggaagagaa	1860
ggggtcattt	atcgcagttt	gggcgtggac	cagaaatgac	tgcagtatgt	ttatggacca	1920
tgccagccgg	agctattgga	ct				1942

&lt;210&gt; 120

&lt;211&gt; 943

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA254; clone 7-1-10; contig 4911 region 43163-41221  
Genomic sequence containing the coding region

&lt;400&gt; 120

atgactaccg	gggctggtac	gatctctcat	tccaacacct	atcatcgat	tcctcgccgt	60
taactgacca	atccaccagt	gcaaagggtt	cgtccagtgg	tggatcggg	tccctctggg	120
actgggaagt	cgaccttgct	caagagactc	ttcgctgaat	accccgatac	tttcgattta	180
tccgtgtctc	gtacgtctaa	ccccttgcca	accctcattg	actatgcctg	cgaattgttt	240
cttttggtgg	aattgcgctg	aacggtgttt	gttatattta	gataccactc	gagctccccg	300
tcccggggaa	gaaaatggac	gtgagtatta	cttcacaact	aaagaagatt	tcctggatct	360
tgtgagcaag	aatgccttta	tcgagcatgc	gcagtttggg	ggcaattact	acggtactac	420
tgtgcaggca	gtgaaggatg	ttgcgcagaa	gggcaagatc	tgcgttctcg	acattgagat	480
ggaggttaata	atagtcctgc	aacgtgaact	gatatgaccg	gagaagcaga	ggaaatccat	540
catcaaattg	attgtagttc	aacccaaaca	acagctgacg	actgaattgc	aatagggcgt	600
gaaacaagtc	aagcgcaccg	atcttgatgc	tcgattctta	tttttagcac	cccgtccct	660
tgaagaacta	gagaaaagac	tgcgtgggag	agcaaccgag	actgaggaga	gcttgacggt	720
atggctgtcc	tccacattcc	ttcacttccc	caactcgcca	gactgtcccc	ctggaattct	780
aactttgcgt	cagaaaacgcc	ttgcccagc	taaaaatgaa	ttggaatatg	cggcgcagcc	840
tggctctcat	gataagattg	tcgtgaacga	tgacctggag	aaggcttata	aggaactgcg	900
ggattggatt	gtcgacgggtg	gtaactttgg	agcgcgtcaa	tga		943

&lt;210&gt; 121

&lt;211&gt; 603

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA254; clone 7-1-10; contig 4911 region 43163-41221  
Coding region without exons

<400> 121

```

atgactaccg gggctgtgca aaggttccgt ccagtgggtg tatcgggtcc ctctgggact    60
gggaagtcga ccttgctcaa gagactcttc gctgaatacc ccgatacttt cgatttatcc    120
gtgtctcata ccaactcgagc tccccgtccc ggggaagaaa atggacgtga gtattacttc    180
acaactaaag aagatttcct ggatcttgtg agcaagaatg cctttatcga gcatgcgcag    240
tttggtgggc attactacgg tactactgtg caggcagtga aggatgttgc gcagaagggc    300
aagatctgcg ttctcgacat tgagatggag ggcgtgaaac aagtcaagcg caccgatctt    360
gatgctcgat tcttattttt agcaccctcg tcccttgaag aactagagaa aagactgcgt    420
gggagagcaa ccgagactga ggagagcttg acgaaacgcc ttgcccaagc taaaaatgaa    480
ttggaatatg cggcgcagcc tggctctcat gataagattg tcgtgaacga tgacctggag    540
aaggcttata aggaactgcg ggattggatt gtcgacggtg gtaactttgg agcgcgtcaa    600
tga                                                    603

```

<210> 122

<211> 200

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA254; clone 7-1-10; contig 4911 region 43163-41221  
Protein sequence

<400> 122

```

Met Thr Thr Gly Ala Val Gln Arg Phe Arg Pro Val Val Val Ser Gly
1          5          10          15

Pro Ser Gly Thr Gly Lys Ser Thr Leu Leu Lys Arg Leu Phe Ala Glu
20          25          30

Tyr Pro Asp Thr Phe Asp Leu Ser Val Ser His Thr Thr Arg Ala Pro
35          40          45

Arg Pro Gly Glu Glu Asn Gly Arg Glu Tyr Tyr Phe Thr Thr Lys Glu
50          55          60

Asp Phe Leu Asp Leu Val Ser Lys Asn Ala Phe Ile Glu His Ala Gln
65          70          75          80

Phe Gly Gly Asn Tyr Tyr Gly Thr Thr Val Gln Ala Val Lys Asp Val
85          90          95

Ala Gln Lys Gly Lys Ile Cys Val Leu Asp Ile Glu Met Glu Gly Val
100         105         110

Lys Gln Val Lys Arg Thr Asp Leu Asp Ala Arg Phe Leu Phe Leu Ala
115         120         125

Pro Pro Ser Leu Glu Glu Leu Glu Lys Arg Leu Arg Gly Arg Ala Thr
130         135         140

Glu Thr Glu Glu Ser Leu Thr Lys Arg Leu Ala Gln Ala Lys Asn Glu
145         150         155         160

```

Leu Glu Tyr Ala Ala Gln Pro Gly Ser His Asp Lys Ile Val Val Asn  
165 170 175

Asp Asp Leu Glu Lys Ala Tyr Lys Glu Leu Arg Asp Trp Ile Val Asp  
180 185 190

Gly Gly Asn Phe Gly Ala Arg Gln  
195 200

<210> 123

<211> 3108

<212> DNA

<213> Aspergillus fumigatus

 $\langle 220 \rangle$ 

<223> Phylum CEA255; clone 10-3-7; contig 4899 region 441274-438167  
Genomic sequence containing 3' and 5'-ends and the coding region

$\langle 400 \rangle$  123

aaaccaggcg	catatgttcc	gctgcgcgcc	tgcgcaggag	agggctgata	aggattgcca	60
tatccagacg	acgggggctg	ctgggatgct	gggggaggag	gcgagcgcat	catgggaacg	120
gtagatacat	gctgaggcac	aggatggtgg	agtggagggtg	actgcgcagg	cggtgggtgcg	180
aaagactggc	ggtacatggt	gatttttttt	tcccttgtta	caataagtga	gaagctagtg	240
atgaacaaaa	gacttgcgac	tattctgtct	cgtcttcttg	tcttctacca	accgaagagg	300
ggggatggtg	gaaatcggac	agtttgagta	tgagtgatgt	tgaagtgtgt	ttatacgtgg	360
ctggactcgg	tctgatcgcc	ggagagctct	caccttttcc	gcccacggtt	ccccaccata	420
gtggccacta	cacacacttg	tccgtttctcc	aaaaccacg	ctgctgcac	tgaataatat	480
acacagaag	tgcttacaac	atggttagaag	ccttcgaagt	cttgacaaca	tctgggtggg	540
tgctgtggtc	gaagtcgat	gcgcgggtcg	gagcgcattgt	tgtcaacagc	ctaatacaacg	600
atgtcttcat	tgaggagaag	gttcgagcgc	agaatcaggc	agcgagcagt	gcagctccta	660
tctacaagaa	ggaaaagtat	actctgaaat	ggaagcaagt	aaaggatttc	aatctgatata	720
ttgtggatatg	ttcacgcgcg	tcgttgattc	aatggcgcca	ctgaccgatt	ccataggctg	780
tatatcaatc	tctgctacat	cttggttgga	tgcacaaact	cttgataat	gtttcgacca	840
tattcatoga	cttatataag	gatgagctaa	ggagcacacg	ggctaggatt	attgagtacc	900
cattcgataa	gtacttcgac	cagcagggtgc	gagagcttga	ggacaatgct	ggggctccta	960
catcagaatc	tctcgtagta	gagatcaacg	agagaaaagg	ccctcttgct	tcatacagata	1020
acggggggcc	acctccgcca	cccgtgcctg	gtctgctgaa	aggtatctga	cgtcgataat	1080
ttttctctgc	tagtgatcat	attgtcaact	acctccgaag	cgcaacgtcc	agttgcgcag	1140
ggcgtggcga	cctcggacga	gggttcgcca	ccccaaaccc	cagatctttc	tcgatcgtca	1200
acgcccattt	caggtcattct	attgaccgcg	aaaggaggggc	ctgctggcgcg	cgctctcgt	1260
cgcgcacgca	aagcggccaa	cgcgagcgt	accgcttctt	ctggagatga	aagcattcgg	1320
aaagggaaaa	cattgaaaag	tggaaaaaag	atgcgcaagt	gggatgctga	tggctttgcg	1380
gatgaggacg	acggcaaggt	cctcgattac	tccgcccccg	cagatggtga	ggacgcaccg	1440
gctcctgtag	tcgaggctgt	tgcgaggaa	tcttggggac	gccgaacagg	caagggccaa	1500
tttgtgctga	aagatctagg	ggatgaagtc	cattccattc	ttgagaatgc	tgatcatgaa	1560
aaagacaaagt	cttcctcgtc	cacgggcttt	gttggtctg	gagtcacgc	acttggtgga	1620
ttcttcctga	atattgtcgg	cggcaagtg	cttactgagg	ctgacttggga	gaaacccctg	1680
aaagccatgg	aagaccattt	gctgaagaag	aacgttgcgc	gcgaagcggc	cgctcgtcta	1740
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gcagcactgc	gctccgcaat	ggagtctctg	ttgcgcaaaa	tattgacgcc	aacgtcatct	1860
ctcgatctac	tgcgtgagat	cgatgctgtt	agatctccga	cgagcaaagg	acaggctcct	1920
cgcccatatg	tcatttccat	cgtgggcgtg	aacggtgttg	ggaagtcgac	aaatctgggc	1980
aaaatttggt	acttccttct	ccagaataac	tatcgtgttc	tgattgcagc	ctgtgacacc	2040
ttccgctctg	gagccgtgga	gcagttacga	gtccatgctc	gcaatttgaa	ggaacttagt	2100
acccggggaga	atgctggaga	ggttgaactc	tacgagaagg	gatattggaaa	ggatgcagcg	2160
aatgtagcga	aggatgcagt	ggagtaacgt	gcggcgaatc	atttcgacgt	tgtgttgatt	2220
gatactgcg	gtcgcgctca	taacgaccaa	cgccttatgt	cttcgctcga	gaagtcgcc	2280
aagttcgcca	aaccagataa	gactttcatg	gtcggtagaag	ctctggtcgg	tacggacagc	2340
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gctacaggca	ttcctattgt	ttttctgggt	gtaggccagc	actatggtga	tttgaggggc	2520
ctaagtgttc	cttgggctgt	caatctgctg	atgaagtgag	cgcgagctt	ttgccttgta	2580
atagagaatt	atattatctc	gcttctgctc	acgctgggtc	ttggatggcc	ttcttcaaaa	2640
ataagttact	gcgattgtac	atctcgcgct	tcgctaaaga	tagagaaacg	aaagatagac	2700
aaagaacggg	ggaaaaaatt	gacaaaaaga	atgacctacg	caggattcga	acctgcaatc	2760
tcttgatccg	tagtcaagcg	ccttaccatt	gggccagcag	gccttcttga	aggttttcac	2820
ccagaaatat	gctttatcag	gaatctggga	acatccgcac	aaactccaat	aataagcttg	2880
tgctgtcat	tgttactacg	ctaaagtgac	tctctagtgt	ggctcttatg	caggagaaac	2940
catacaggat	attgtaacgg	tgaatgcatt	ttttctgcct	tgaggatatga	caccattttg	3000
ttttggagggt	ggactcgatc	acgagctcac	tatcccgccc	tcatgggagg	attatgacac	3060
ccttggttcc	tgaatacttg	gtcttggtcg	gaattacttc	aatgacac		3108

&lt;210&gt; 124

&lt;211&gt; 2059

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA255; clone 10-3-7; contig 4899 region 441274-438167  
 Genomic sequence containing the coding region

&lt;400&gt; 124

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gcgccggtcg	gagcgcattg	tgtcaacagc	ctaatacaacg	atgtcttcat	tgaggagaag	120
gttcgagcgc	agaatcaggc	agcgagcagt	gcagctccta	tctacaagaa	ggaaaagtat	180
actctgaaat	ggaagcaagt	aaaggatttc	aatctgatat	ttgtggtatg	ttcacgccgc	240
tcgttgattc	aatggcgcca	ctgaccgatt	ccataggctg	tatatcaatc	tctgctacat	300
cttggttgga	tcgacaaaact	cttggataat	gtttcgacca	tattcatcga	cttatataag	360
gatgagctaa	ggagcacacg	ggctaggatt	attgagtacc	cattcgataa	gtacttcgac	420
cagcaggtgc	gagagcttga	ggacaatgct	ggggctccta	catcagaatc	tctcgtagta	480
gagatcaacg	agagaaaagga	ccctcttgtc	tcatacagata	acggcggggc	acctccgcca	540
cccgtgcctg	gtctgctgaa	aggtatctga	cgctcgataat	ttttctctgc	tagtgatcat	600
attgctaact	acctccgaag	cgcaacgtcc	agttgcgcag	ggcgtggcga	cctcggacga	660
gggttcgcca	ccccaaaccc	cagatctttc	tcgatcgtca	acgcccatct	caggtcattc	720
attgaccgcg	aaaggagggg	ctgctggccg	cgctctctgt	cgcgcacgca	aagcggccaa	780
cgcgagcgct	accgcttctt	ctggagatga	aagcattcgg	aaggggaaaa	cattgaaaag	840
tggaaaaaag	atgcgcaagt	gggatgctga	tggtcttgcg	gatgaggacg	acggcaagggt	900
cctcgattac	tccgcccccg	cagatgggtga	ggacgcaccg	gctcctgtag	tcgaggctgt	960
tgcgacggaa	tccgtgggac	gccgaacagg	caagggccaa	tttgtgctga	aagatctagg	1020
ggatgaagtc	cattccattc	ttgagaatgc	tgatcatgaa	aagacaaaagt	cttcctcgtc	1080
cacgggcttt	gttgggtctg	gagtcaacgc	acttggtgga	ttcttccgta	atattgtcgg	1140
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gctgaagaag	aacgttgcg	gcgaagcggc	cgtccgtcta	tgtcaaggcg	tccagcgcga	1260
attagttggc	agaagacag	gcaactttca	aagtgttgat	gcagcactgc	gctccgcaat	1320
ggagtcctcg	ttgcgcaaaa	tattgacgcc	aacgtcatct	ctcgatctac	tgcgtagagat	1380
cgatgctggt	agatctccga	cgagcaaaag	acaggctcct	cgcccatatg	tcatttccat	1440
cgtgggcgtg	aacgggtgtg	ggaagtcgac	aaatctgggc	aaaatttggt	acttccttct	1500
ccagaataac	tatcgtgttc	tgattgcagc	ctgtgacacc	ttccgctctg	gagccgtgga	1560
gcagttacga	gtccatgctc	gcaatttgaa	ggaacttagt	acccggggaga	atgctggaga	1620
ggttgaactc	tacgagaagg	gatatggaaa	ggatgcagcg	aatgtagcga	aggatgcagt	1680
ggagtacggg	gcggcgaatc	atttcgacgt	tgtgttgatt	gatactgccg	gtcgccgtca	1740
taacgaccaa	cgccttatgt	cttcgctcga	gaagttcgcc	aagttcgcca	aaccagataa	1800
gatcttcatg	gtcgggtgaag	ctctggtcgg	tacggacagc	gtgatgcagg	ctcgcaactt	1860
caaccaagct	ttcggcactg	ggagaaaacct	cgatgggttc	atcatcagta	aatgtgatac	1920
cgttgggtgac	atggtaggta	cgcttgtcag	catggtgcat	gtacacaggca	ttcctattgt	1980
ttttctgggt	gtaggccagc	actatggtga	tttgaggggc	ctaagtgttc	cttgggctgt	2040
caatctgctg	atgaagtga					2059

<210> 125  
 <211> 1884  
 <212> DNA  
 <213> *Aspergillus fumigatus*

<220>  
 <223> Phylum CEA255; clone 10-3-7; contig 4899 region 441274-438167  
 Coding region without exons

<400> 125  
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 gcgcgggtcg gagcgcatgt tgtcaacagc ctaatcaacg atgtcttcat tgaggagaag 120  
 gttcgaagcg agaatacagg agcgagcagt gcagctccta tctacaagaa ggaaaagtat 180  
 actctgaaat ggaagcaagt aaaggatttc aatctgatat ttgtgcttgg ttggatcgac 240  
 aaactcttgg ataattgtttc gaccatattc atcgacttat ataaggatga gctaaggagc 300  
 acacgggcta ggattattga gtacccattc gataagtact tcgaccagca ggtgcgagag 360  
 cttgaggaca atgctggggc tcctacatca gaatctctcg tagtagagat caacgagaga 420  
 aaggaccctc ttgtctcatc agataacggc gggccacctc cgccacccgt gcctgcctcg 480  
 gacgaggggtt cgccacccca aaccccagat ctttctcgat cgtcaacgcc catttcaggt 540  
 catctattga ccgcgaaaag agggcctgct ggccgcgcct ctcgtcgcgc acgcaaagcg 600  
 gccaacgcga gcgctaccgc ttcttctgga gatgaaagca ttcggaagg gaaaacattg 660  
 aaaagtggaa aaaagatgcg caagtgggat gctgatggct ttgcggatga ggacgacggc 720  
 aaggctcctcg attactccgc cccgcgagat ggtgaggacg caccggctcc tgtagtcgag 780  
 gctgttgcgc aggaatcctg gggacgccga acaggcaagg gccaatattgt gctgaaagat 840  
 ctaggggatg aagtccattc cattcttgag aatgctgac atgaaaagac aaagtcttcc 900  
 tcgtccacgg gctttgttgg gtctggagtc aacgcacttg gtggattctt ccgtaatat 960  
 gtgcggcgca aggtccttac tgaggctgac ttggagaaac ccttgaaaagc catggaagac 1020  
 catttgctga agaagaacgt tgcgcgcgaa gcggccgtcc gtctatgtca aggcgtccag 1080  
 cgcgaaattag ttggcaagaa gacaggcaac tttaaagtgt ttgatgcagc actgcgtcc 1140  
 gcaatggagt cctcgttgcg caaaatattg acgccaacgt catctctcga tctactgcgt 1200  
 gagatcgatg ctgttagatc tccgacgagc aaaggacagg ctctcgcgcc atatgtcatt 1260  
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 gataccgttg tgcacatggt aggtacgctt gtcagcatgg tgcattgctac aggcattcct 1800  
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<210> 126  
 <211> 641  
 <212> PRT  
 <213> *Aspergillus fumigatus*

<220>  
 <223> Phylum CEA255; clone 10-3-7; contig 4899 region 441274-438167  
 Protein sequence

<400> 126

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Ser Lys Ser Tyr Ala Pro Val Gly Ala His Val Val Asn Ser Leu Ile  
 20 25 30

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Ser	Ser	Ala	Ala	Pro	Ile	Tyr	Lys	Lys	Glu	Lys	Tyr	Thr	Leu	Lys	Trp	
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Lys	Gln	Val	Lys	Asp	Phe	Asn	Leu	Ile	Phe	Val	Ala	Val	Tyr	Gln	Ser	
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Leu	Leu	His	Leu	Gly	Trp	Ile	Asp	Lys	Leu	Leu	Asp	Asn	Val	Ser	Thr	
				85					90					95		
Ile	Phe	Ile	Asp	Leu	Tyr	Lys	Asp	Glu	Leu	Arg	Ser	Thr	Arg	Ala	Arg	
			100					105					110			
Ile	Ile	Glu	Tyr	Pro	Phe	Asp	Lys	Tyr	Phe	Asp	Gln	Gln	Val	Arg	Glu	
		115					120					125				
Leu	Glu	Asp	Asn	Ala	Gly	Ala	Pro	Thr	Ser	Glu	Ser	Leu	Val	Val	Glu	
	130					135					140					
Ile	Asn	Glu	Arg	Lys	Asp	Pro	Leu	Val	Ser	Ser	Asp	Asn	Gly	Gly	Pro	
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Pro	Pro	Pro	Pro	Val	Pro	Val	Ala	Gln	Gly	Val	Ala	Thr	Ser	Asp	Glu	
				165					170					175		
Gly	Ser	Pro	Pro	Gln	Thr	Pro	Asp	Leu	Ser	Arg	Ser	Ser	Thr	Pro	Ile	
			180					185					190			
Ser	Gly	His	Leu	Leu	Thr	Ala	Lys	Gly	Gly	Pro	Ala	Gly	Arg	Ala	Ser	
		195					200					205				
Arg	Arg	Ala	Arg	Lys	Ala	Ala	Asn	Ala	Ser	Ala	Thr	Ala	Ser	Ser	Gly	
	210					215					220					
Asp	Glu	Ser	Ile	Arg	Lys	Gly	Lys	Thr	Leu	Lys	Ser	Gly	Lys	Lys	Met	
225					230					235					240	
Arg	Lys	Trp	Asp	Ala	Asp	Gly	Phe	Ala	Asp	Glu	Asp	Asp	Gly	Lys	Val	
				245					250					255		
Leu	Asp	Tyr	Ser	Ala	Pro	Ala	Asp	Gly	Glu	Asp	Ala	Pro	Ala	Pro	Val	
			260					265				270				
Val	Glu	Ala	Val	Ala	Gln	Glu	Ser	Trp	Gly	Arg	Arg	Thr	Gly	Lys	Gly	
		275					280					285				
Gln	Phe	Val	Leu	Lys	Asp	Leu	Gly	Asp	Glu	Val	His	Ser	Ile	Leu	Glu	
	290					295					300					
Asn	Ala	Asp	His	Glu	Lys	Thr	Lys	Ser	Ser	Ser	Ser	Thr	Gly	Phe	Val	
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Gly	Ser	Gly	Val	Asn	Ala	Leu	Gly	Gly	Phe	Phe	Arg	Asn	Ile	Val	Gly	
				325					330					335		
Gly	Lys	Val	Leu	Thr	Glu	Ala	Asp	Leu	Glu	Lys	Pro	Leu	Lys	Ala	Met	
			340					345					350			
Glu	Asp	His	Leu	Leu	Lys	Lys	Asn	Val	Ala	Arg	Glu	Ala	Ala	Val	Arg	

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Phe Gln Ser Val Asp Ala Ala Leu Arg Ser Ala Met Glu Ser Ser Leu 385 390 395 400		
Arg Lys Ile Leu Thr Pro Thr Ser Ser Leu Asp Leu Leu Arg Glu Ile 405 410 415		
Asp Ala Val Arg Ser Pro Thr Ser Lys Gly Gln Ala Pro Arg Pro Tyr 420 425 430		
Val Ile Ser Ile Val Gly Val Asn Gly Val Gly Lys Ser Thr Asn Leu 435 440 445		
Gly Lys Ile Cys Tyr Phe Leu Leu Gln Asn Asn Tyr Arg Val Leu Ile 450 455 460		
Ala Ala Cys Asp Thr Phe Arg Ser Gly Ala Val Glu Gln Leu Arg Val 465 470 475 480		
His Ala Arg Asn Leu Lys Glu Leu Ser Thr Arg Glu Asn Ala Gly Glu 485 490 495		
Val Glu Leu Tyr Glu Lys Gly Tyr Gly Lys Asp Ala Ala Asn Val Ala 500 505 510		
Lys Asp Ala Val Glu Tyr Gly Ala Ala Asn His Phe Asp Val Val Leu 515 520 525		
Ile Asp Thr Ala Gly Arg Arg His Asn Asp Gln Arg Leu Met Ser Ser 530 535 540		
Leu Glu Lys Phe Ala Lys Phe Ala Lys Pro Asp Lys Ile Phe Met Val 545 550 555 560		
Gly Glu Ala Leu Val Gly Thr Asp Ser Val Met Gln Ala Arg Asn Phe 565 570 575		
Asn Gln Ala Phe Gly Thr Gly Arg Asn Leu Asp Gly Phe Ile Ile Ser 580 585 590		
Lys Cys Asp Thr Val Gly Asp Met Val Gly Thr Leu Val Ser Met Val 595 600 605		
His Ala Thr Gly Ile Pro Ile Val Phe Leu Gly Val Gly Gln His Tyr 610 615 620		
Gly Asp Leu Arg Gly Leu Ser Val Pro Trp Ala Val Asn Leu Leu Met 625 630 635 640		
Lys		

&lt;210&gt; 127

&lt;211&gt; 2564

&lt;212&gt; DNA

&lt;213&gt; Aspergillus fumigatus



&lt;220&gt;

<223> Phylum CEA256; clone 2-6-4; contig 4938 region 582107-579544  
Genomic sequence containing 3' and 5'-ends and the coding region

&lt;400&gt; 127

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tggattggat	caaggattca	attgatcaga	gctcggctca	gatcatgtat	ccagtcttcc	180
gatgattccg	attattgtga	aactgggtta	aatcgcgcca	gaggggcagg	tatcgtgacg	240
gagagggggg	atatcgtcga	atggagggtg	tgagtgcaga	cggccgacga	ttgcgcagtt	300
caaagcggcg	aagaggtctt	ggcactctcg	gtccaaacac	gttgcccgtt	ctctccaact	360
aaacggaact	gacgaagctc	cttcagagga	cactctcctc	taccgattca	tttctttaat	420
ctattccttc	tctttctccg	gactgcagtg	acttcccttt	cagccaattg	cccgtctccac	480
tgtgcggcat	tcgatatacc	atgcggtggt	gcctcactct	tctggcattc	tgcttcttgg	540
cagttgtacg	tgcattaagt	agctccggca	gtcgtctggt	ggttgttttg	gaagatgcca	600
cagaaaagga	attatactcg	aaattatggg	ctgacctaga	aggtgctcta	acctactgaa	660
cttctacgtt	aatatgctaa	tattaattgg	tagctcgagg	atataacctc	gacttcgaat	720
cccccaagaa	tgacaagctc	agcctgttcg	aactcggaga	ccgagtctac	gaccacatgc	780
ttctcctgcc	tcccaagtca	aagggttagc	gttaccctta	gacatgtcca	tatgctctgc	840
tttgtacatc	tcaattgacc	tcttggccag	gctatggacc	ctcccttacc	cccaagaata	900
tcattgattt	catgaacaag	gacggtaacg	tcctctcgcg	cttgtcgggc	aagtccacaa	960
ccgccagcgc	tatcagctcg	ctgctattgg	agctcgatct	ccatctccct	gtcgatcggt	1020
cctctgtcac	cgtcgatcac	ttcaactacg	atacactttc	tgcttccgat	aagcatgatg	1080
ttctgctact	ccaccgacca	ggcaagttga	ggtccgatac	caaggctttc	tttgateggcg	1140
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ttgcgcctat	tctgcgagcg	cccgccactg	cgtatagtta	caaccccaag	gaggacgcgt	1260
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gaagcgtgca	cttacgcggg	aagcccataa	ttcaaaaagta	tgtacagtca	tatgccataa	2160
gctagtagtg	ttacatgaaa	tccggaatct	caagacattc	cgccaactgg	gaactccaaa	2220
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catctgaact	tcattcccgc	tgatctcctt	aacggtttcg	aaggcgggct	tgccggcgta	2400
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atttccacgg	aatcgctttc	gcattgtgat	caaccacgcg	ctagattgtg	cccgttgtca	2520
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&lt;210&gt; 128

&lt;211&gt; 1564

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA256; clone 2-6-4; contig 4938 region 582107-579544  
Genomic sequence containing the coding region

&lt;400&gt; 128

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aaattatggg	ctgacctaga	aggtgctcta	acctactgaa	cttctacgtt	aatatgctaa	180
tattaattgg	tagctcgagg	atataacctc	gacttcgaat	cccccaagaa	tgacaagctc	240
agcctgttcg	aactcggaga	ccgagtctac	gaccacatgc	ttctcctgcc	tcccaagtca	300
aagggttagc	gttaccctta	gacatgtcca	tatgctctgc	tttgtacatc	tcaattgacc	360
tcttgccag	gctatggacc	ctcccttacc	ccaagaata	tcattgattt	catgaacaag	420
gacggtaacg	tcctcctcgc	cttgctgggc	aagtccacaa	ccgccagcgc	tatcagctcg	480
ctgctattgg	agctcgatct	ccatctccct	gtcgatcggt	cctctgtcac	cgctgatcac	540
ttcaactacg	atacactttc	tgccctcgat	aagcatgatg	ttctgtact	ccaccgacca	600
ggcaagttga	ggtccgatac	caaggctttc	tttgatggcg	agggcggtgt	agcatttccc	660
agagccgtcc	cccacaccct	gggcgatgca	aacctctca	ttgcgcctat	tctgcgagcg	720
cccgccactg	cgtatagtta	caaccccaag	gaggacgcgt	cgtcagttga	ggatgttgca	780
gctacggggt	cgagttggc	tctgggtctcg	gccatgcagg	ctagaaactc	cgctcgggtc	840
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cctggtgatg	ggaagcagat	gaagacggtc	aaccaggaat	tcgccaagca	gcttactgcg	960
tggacattca	aggaaaccgg	agtcctcaag	gtcggaaaaga	tcgagcatca	tctggctgaa	1020
gatggtgaaa	tcactcccga	gaagctgaac	cctaagatct	atcgaataaa	gaatgaaact	1080
gtaagtgaca	gccatctgag	gttccattgc	ctatttgcat	gtcaccctt	ctcaacaggt	1140
cttttagcatt	gaactttccg	aatacaacta	tgatcggttac	gcgcccttcg	aggttccaac	1200
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accggtccgt	cgaacagata	acagtacagt	ttacagcaca	cgattcacca	ccccgatca	1320
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aaaacttgag	gtgaccgttc	gtcattttgc	tcataacgag	tacccccgaa	gctggaaaat	1440
cagcggtgga	tgggtctgga	ttgcgggtct	gtggtccgtc	atcgctggct	tcttagtatt	1500
cgttgttgca	tggctttact	cagcgccttc	tgccgccgca	ctgaacacaa	agaagacaca	1560
ataa						1564

&lt;210&gt; 129

&lt;211&gt; 1383

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA256; clone 2-6-4; contig 4938 region 582107-579544  
Coding region without exons

&lt;400&gt; 129

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aaattatggg	ctgacctaga	aggatataac	ctcgacttcg	aatcccccaa	gaatgacaag	180
ctcagcctgt	tcgaactcgg	agaccgagtc	tacgaccaca	tgcttctcct	gcctoccaaag	240
tcaaagggct	atggaccctc	ccttaccccc	aagaatatca	ttgatttcat	gaacaaggac	300
ggtaacgtcc	tcctcgcctt	gtcgggcaag	tccacaaccg	ccagcgctat	cagctcgctg	360
ctattggagc	tcgatctcca	tctccctgtc	gatcgttcct	ctgtcaccgt	cgatcacttc	420
aactacgata	cacttttctgc	ctccgataag	catgatgttc	tgctactcca	ccgaccaggc	480
aagttgaggt	ccgataccaa	ggcttttctt	gatggcgagg	gcgttgtagc	atttcccaga	540
gccgtccccc	acaccctggg	cgatgcaaac	cctctcattg	cgctatttct	gcgagcgccc	600
gccactgcgt	atagttacaa	ccccaggag	gacgcgtcgt	cagttgagga	tggtgcagct	660
acgggttcgc	agttggctct	ggtctcggcc	atgcaggcta	gaaactccgc	tcggttcact	720
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acattcaagg	aaaccggagt	cctcaaggtc	ggaaagatcg	agcatcatct	ggctgaagat	900
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ggcgatgccg	tccagctcga	gtttaccatg	ctgtctccct	tccatcgccct	gaacttgga	1080
cccgtccgtc	gaacagataa	cagtacagtt	tacagcacac	gattcaccac	ccccgatcag	1140
catggaatct	tctccttccg	agtgaactac	aagcgcccg	tcctcacgaa	catcgaagaa	1200
aaacttgagg	tgaccgttcg	tcatttctgt	cataacgagt	acccccgaag	ctggaaaatc	1260
agcgggtggat	gggtctggat	tgcgggtctg	tggtccgtca	tcgctggctt	cttagtatct	1320

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taa 1383

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<210> 130
<211> 460
<212> PRT
<213> Aspergillus fumigatus
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<220>
<223> Phylum CEA256; clone 2-6-4; contig 4938 region 582107-579544
      Protein sequence
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Ala	Thr	Glu 35	Lys	Glu	Leu	Tyr	Ser 40	Lys	Leu	Trp	Ala	Asp 45	Leu	Glu	Gly
Tyr	Asn 50	Leu	Asp	Phe	Glu	Ser 55	Pro	Lys	Asn	Asp	Lys 60	Leu	Ser	Leu	Phe
Glu 65	Leu	Gly	Asp	Arg	Val 70	Tyr	Asp	His	Met	Leu 75	Leu	Leu	Pro	Pro	Lys 80
Ser	Lys	Gly	Tyr	Gly 85	Pro	Ser	Leu	Thr	Pro 90	Lys	Asn	Ile	Ile	Asp 95	Phe
Met	Asn	Lys	Asp 100	Gly	Asn	Val	Leu	Leu 105	Ala	Leu	Ser	Gly	Lys 110	Ser	Thr
Thr	Ala	Ser 115	Ala	Ile	Ser	Ser	Leu 120	Leu	Leu	Glu	Leu	Asp 125	Leu	His	Leu
Pro	Val 130	Asp	Arg	Ser	Ser	Val 135	Thr	Val	Asp	His	Phe 140	Asn	Tyr	Asp	Thr
Leu 145	Ser	Ala	Ser	Asp	Lys 150	His	Asp	Val	Leu	Leu 155	Leu	His	Arg	Pro	Gly 160
Lys	Leu	Arg	Ser	Asp 165	Thr	Lys	Ala	Phe	Phe 170	Asp	Gly	Glu	Gly	Val 175	Val
Ala	Phe	Pro	Arg 180	Ala	Val	Pro	His	Thr 185	Leu	Gly	Asp	Ala	Asn 190	Pro	Leu
Ile	Ala	Pro 195	Ile	Leu	Arg	Ala	Pro 200	Ala	Thr	Ala	Tyr	Ser 205	Tyr	Asn	Pro
Lys	Glu 210	Asp	Ala	Ser	Ser	Val 215	Glu	Asp	Val	Ala	Ala 220	Thr	Gly	Ser	Gln
Leu 225	Ala	Leu	Val	Ser	Ala 230	Met	Gln	Ala	Arg	Asn 235	Ser	Ala	Arg	Phe	Thr 240
Leu	Leu	Gly	Ser	Val 245	Glu	Ser	Leu	Gln	Asp 250	Gln	Trp	Phe	Ser	Ala 255	Thr

Val Lys Ala Pro Gly Asp Gly Lys Gln Met Lys Thr Val Asn Gln Glu  
260 265 270

Phe Ala Lys Gln Leu Thr Ala Trp Thr Phe Lys Glu Thr Gly Val Leu  
275 280 285

Lys Val Gly Lys Ile Glu His His Leu Ala Glu Asp Gly Glu Ile Thr  
290 295 300

Pro Glu Lys Leu Asn Pro Lys Ile Tyr Arg Ile Lys Asn Glu Thr Val  
305 310 315 320

Phe Ser Ile Glu Leu Ser Glu Tyr Asn Tyr Asp Arg Tyr Ala Pro Phe  
325 330 335

Glu Val Pro Thr Gly Asp Ala Val Gln Leu Glu Phe Thr Met Leu Ser  
340 345 350

Pro Phe His Arg Leu Asn Leu Glu Pro Val Arg Arg Thr Asp Asn Ser  
355 360 365

Thr Val Tyr Ser Thr Arg Phe Thr Thr Pro Asp Gln His Gly Ile Phe  
370 375 380

Ser Phe Arg Val Asn Tyr Lys Arg Pro Phe Leu Thr Asn Ile Glu Glu  
385 390 395 400

Lys Leu Glu Val Thr Val Arg His Phe Ala His Asn Glu Tyr Pro Arg  
405 410 415

Ser Trp Lys Ile Ser Gly Gly Trp Val Trp Ile Ala Gly Leu Trp Ser  
420 425 430

Val Ile Ala Gly Phe Leu Val Phe Val Val Ala Trp Leu Tyr Ser Ala  
435 440 445

Pro Ser Ala Ala Ala Leu Asn Thr Lys Lys Thr Gln  
450 455 460

<210> 131

<211> 3376

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA257; clone 2-1-1; contig 4951 region 8362-11737  
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 131

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cagactaact	cctgggagac	ggagatgttt	tcttctccga	aagctctctc	tcagtgatgc	360
gggcaggaga	aacgtaacgc	cggcgagatc	ccttttgagt	cagatgcccc	tctgtactat	420
tcaattttcg	gggaattcaa	cagcccaactt	gttacgctct	cgcaggtcga	tttcaactcg	480
ggcgattttt	gagggccgca	atgtctcagt	atcagcttac	tgtggccacc	agggccaatc	540

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cagtgatatc	gatcacctat	gaggatactg	cggttcttcg	tgaaggagac	aaggccgtcg	660
tgcaatacac	tggagctagc	ggtaatccta	tctttggcct	tatcaatgct	gttcagggaac	720
tccgcaaaga	cttccccttc	cttaacagca	aggatgagaa	gctggtaaga	ggcgccatgg	780
agccttactg	ctgatgagca	ctgataagtg	atactaacc	tccttttata	ggagaatgaa	840
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cagcgccctg	ataccacact	cctgctgaga	tctttcgtcg	tcggttacgc	tctctcgacg	960
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&lt;210&gt; 132

&lt;211&gt; 2376

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA257; clone 2-1-1; contig 4951 region 8362-11737  
 Genomic sequence containing the coding region

&lt;400&gt; 132

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60

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&lt;210&gt; 133

&lt;211&gt; 2148

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA257; clone 2-1-1; contig 4951 region 8362-11737  
Coding region without exons

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<210> 134

<211> 715

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA257; clone 2-1-1; contig 4951 region 8362-11737  
Protein sequence

<400> 134

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Val Leu Pro Val Leu Leu Val Ala Thr Ser Ile Asn Glu Ala Arg Pro  
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Ser Pro Val Ile Ser Ile Thr Tyr Glu Asp Thr Ala Val Leu Arg Glu  
35 40 45

Gly Asp Lys Ala Val Val Gln Tyr Thr Gly Ala Ser Gly Asn Pro Ile  
50 55 60

Phe Gly Leu Ile Asn Ala Val Gln Glu Leu Arg Lys Asp Phe Pro Phe  
65 70 75 80

Leu Asn Ser Lys Asp Glu Lys Leu Glu Asn Glu Trp Leu Ser Gln Leu  
85 90 95

Glu Ala Phe Ala Pro Leu Asp Phe Lys Ala Leu Asp Pro Glu Leu Gln  
100 105 110

Arg Leu Asp Thr His Leu Leu Leu Arg Ser Phe Val Val Gly Tyr Ala

115					120					125					
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130						135					140				
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145					150					155					160
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Glu	Gly	Ala	Ser	Tyr	Asp	Ile	Ala	Leu	Leu	Asn	Thr	Glu	Lys	Gly	Val
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Val	Thr	Arg	Phe	Pro	Pro	Glu	Pro	Ser	Gly	Tyr	Leu	His	Ile	Gly	His
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Leu	Glu	Phe	Gln	Asp	Ala	Ile	Ile	Glu	Asp	Leu	Ala	Leu	Met	Gly	Ile
			260					265					270		
Lys	Pro	Asp	Lys	Met	Ser	Tyr	Thr	Ser	Asp	Tyr	Phe	Asp	Glu	Leu	Tyr
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Gln	Tyr	Ala	Leu	Gln	Ile	Ile	Lys	Asp	Gly	Asn	Ala	Tyr	Ala	Asp	Asp
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Thr	Glu	Lys	Glu	Val	Met	Ala	Glu	Gln	Arg	Met	Asn	Gly	Lys	Pro	Ser
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Lys	Arg	Arg	Asp	Ala	Ser	Val	Glu	Glu	Asn	Leu	Ala	Arg	Phe	Glu	Glu
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Met	Lys	Lys	Gly	Thr	Pro	Glu	Gly	Leu	Arg	Trp	Cys	Ile	Arg	Ala	Lys
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Met	Ser	Val	Asp	Asn	Pro	Asn	Lys	Ala	Met	Arg	Asp	Pro	Val	Ile	Tyr
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Arg	Cys	Asn	Pro	Ala	Pro	His	His	Arg	Thr	Gly	Thr	Lys	Trp	Lys	Ile
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Val	Thr	His	Ala	Leu	Arg	Thr	Ile	Glu	Tyr	Arg	Asp	Arg	Asn	Pro	Gln
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			420					425					430		
Asp	Phe	Ala	Arg	Met	Asn	Phe	Ile	Arg	Thr	Leu	Leu	Ser	Lys	Arg	Lys
		435					440					445			



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 465 470 475 480  
 Ala Leu Arg Glu Phe Ile Leu Lys Gln Gly Pro Ser Lys Asn Ile Thr  
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 Asn Leu Asp Trp Thr Leu Ile Trp Ala Thr Asn Lys Lys Tyr Ile Asp  
 500 505 510  
 Pro Val Ala Pro Arg His Thr Ala Ile Leu Lys Lys Asp Met Val Lys  
 515 520 525  
 Ala Ile Val Lys Gly Gly Pro Ala Thr Pro Tyr Thr Glu Glu Lys Pro  
 530 535 540  
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 545 550 555 560  
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 565 570 575  
 Glu Glu Ile Thr Leu Met Ser Trp Gly Asn Ala Ile Val Arg Lys Ile  
 580 585 590  
 Glu Thr Asp Pro Thr Ser Gly Ile Val Lys Glu Leu Glu Leu Glu Leu  
 595 600 605  
 His Leu Glu Gly Asp Phe Lys Lys Thr Glu Lys Lys Val Thr Trp Leu  
 610 615 620  
 Ser Thr Glu Gly Gln Asp Leu Ile Pro Val Glu Leu Val Asp Phe Asp  
 625 630 635 640  
 Tyr Leu Leu Asn Lys Asp Thr Leu Gln Glu Asp Asp Val Leu Glu Asp  
 645 650 655  
 Val Leu Asn Lys Asn Thr Glu Phe Arg Glu Asp Ala Val Ala Asp Cys  
 660 665 670  
 Asn Val Ala Glu Leu Lys Glu Gly Asp Ile Ile Gln Phe Glu Arg Lys  
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<210> 135

<211> 3639

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA258; clone 2-10-16; contig 4912 region 46084-42446  
 Genomic sequence containing 3' and 5'-ends and the coding region

&lt;400&gt; 135

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<210> 136

<211> 2639

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA258; clone 2-10-16; contig 4912 region 46084-42446  
Genomic sequence containing the coding region

<400> 136

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<211> 2430  
 <212> DNA  
 <213> *Aspergillus fumigatus*

<220>  
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 <213> *Aspergillus fumigatus*

<220>  
 <223> Phylum CEA258; clone 2-10-16; contig 4912 region 46084-42446  
 Protein sequence

<400> 138

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 50 55 60  
 Tyr Ser Arg Asn Phe Gly Ser Arg Gly Thr His Leu Gly Cys Ser Tyr  
 65 70 75 80  
 Val Phe Ala Gln Ala Cys Leu Asp Leu Gly Lys Tyr Leu Glu Gly Ile  
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 Thr Ala Leu Glu Arg Ser Lys Gly Leu Trp Ala Ser Lys Asn His Trp  
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 Asn Lys His Ser Glu Thr Arg Arg Gln His Leu Pro Asp Ala Ala Ala  
 115 120 125  
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 Lys Ala Val Glu Cys Tyr Val Glu Ser Leu Lys Leu Asn Pro Phe Met  
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 Ser Asn Ile Tyr Lys Leu Asn Ser Glu Leu Leu Ala Val Leu Ser Ser  
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 195 200 205  
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 245 250 255  
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<213> Aspergillus fumigatus
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<223> Phylum CEA259; clone 5-4-21; contig 4963 region 373462-376145
Genomic sequence containing 3' and 5'-ends and the coding region
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&lt;211&gt; 1707

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

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<223> Phylum CEA259; clone 5-4-21; contig 4963 region 373462-376145  
Genomic sequence containing the coding region

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ctggagaagg	cggagtgcgc	cgttcatacc	tgcccttggg	acaactgcac	gaaattccgg	1320



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gcaccgcagt	acaacgggct	ttcatggaag	aaagccgtct	tccttagtca	tcgtccaaag	1620
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gtaatagaaa	aagaggatta	ttactga				1707

&lt;210&gt; 141

&lt;211&gt; 1707

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA259; clone 5-4-21; contig 4963 region 373462-376145  
Coding region without exons

&lt;400&gt; 141

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ctgttgagga	agatcaaaca	aatgccagtt	acattgccgg	aagacaccct	cgagacgtac	180
gaattcaacc	accttctgcg	caacgttaaa	gaagcgaccc	tggtactacg	caatatggtc	240
cttctgaaag	agaatgccta	ctatgtgtca	cggtacgcga	aaggcctgct	ccgagacttc	300
ctcgtcatta	tgatcaactt	gcccacacag	cctcgtctca	acgagatcaa	gaacgacgct	360
ttggacattg	cagaggaggt	caccaagttt	atgaagaccg	atccggaaga	tccacttttg	420
atctcacttc	tcaattgtct	cgggtcgtca	gatcgtgctc	acgtgggtccg	cgcactctgg	480
gctctcacc	atttctccac	tgaattagac	gagccagagg	cgaaccgggc	aatggaacgg	540
ataccaaaag	agactttgca	gcagctctac	tttcacactc	ttctcgactt	ggacaaagat	600
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gcgcaagcac	aggtgatcaa	tggccctggg	gcagccacga	aattcatcat	caaaggcatt	1080
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ctggagaagg	cggagtcgcc	cgttcatacc	tgcttttggg	acaactgcac	gaaattccgg	1320
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gcaccgcagt	acaacgggct	ttcatggaag	aaagccgtct	tccttagtca	tcgtccaaag	1620
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&lt;210&gt; 142

&lt;211&gt; 568

&lt;212&gt; PRT

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA259; clone 5-4-21; contig 4963 region 373462-376145  
Protein sequence

&lt;400&gt; 142

Met	Ala	Lys	Ala	Leu	Asp	Ile	Ser	Leu	Val	Thr	Thr	Gly	Val	Lys	Trp	1	5	10	15
Glu	Leu	Gln	Tyr	Asp	Val	Leu	Gln	Leu	Ser	Asp	Arg	Val	Asn	Glu	Leu	20	25	30	
Asn	Ser	Leu	His	Gly	Thr	Arg	Asp	Leu	Leu	Glu	Lys	Ile	Lys	Gln	Met	35	40	45	
Pro	Val	Thr	Leu	Pro	Glu	Asp	Thr	Leu	Glu	Thr	Tyr	Glu	Phe	Asn	His	50	55	60	
Leu	Leu	Arg	Asn	Val	Lys	Glu	Ala	Thr	Leu	Val	Leu	Arg	Asn	Met	Val	65	70	75	80
Leu	Leu	Lys	Glu	Asn	Ala	Tyr	Tyr	Val	Ser	Arg	Tyr	Ala	Lys	Gly	Leu	85	90	95	
Leu	Arg	Asp	Phe	Leu	Val	Ile	Met	Ile	Asn	Leu	Pro	Asn	Gln	Pro	Arg	100	105	110	
Leu	Asn	Glu	Ile	Lys	Asn	Asp	Ala	Leu	Asp	Ile	Ala	Glu	Glu	Val	Thr	115	120	125	
Lys	Phe	Met	Lys	Thr	Asp	Pro	Glu	Asp	Pro	Leu	Trp	Ile	Ser	Leu	Leu	130	135	140	
Asn	Cys	Leu	Gly	Ser	Ser	Asp	Arg	Ala	His	Val	Val	Arg	Ala	Leu	Trp	145	150	155	160
Ala	Leu	Thr	His	Phe	Ser	Thr	Glu	Leu	Asp	Glu	Pro	Glu	Ala	Asn	Arg	165	170	175	
Ala	Met	Glu	Arg	Ile	Pro	Lys	Glu	Thr	Leu	Gln	Gln	Leu	Tyr	Phe	His	180	185	190	
Thr	Leu	Leu	Asp	Leu	Asp	Lys	Asp	Ile	Leu	Ser	Gly	Ala	Leu	Asp	Phe	195	200	205	
Trp	Tyr	Gln	Tyr	Thr	Leu	Ser	Ser	Glu	Asn	Ile	Glu	Thr	Leu	Ile	Glu	210	215	220	
Val	Phe	Asn	Leu	Pro	Thr	Val	Phe	Val	Pro	Arg	Met	Val	Ala	Leu	Leu	225	230	235	240
Thr	His	Glu	Gly	Arg	Pro	Asn	Lys	Lys	Glu	Thr	Val	Leu	Gln	Glu	Glu	245	250	255	
Lys	Val	Ala	Pro	Pro	Pro	Ser	Asp	Ile	Pro	Arg	Val	Pro	Pro	Glu	Leu	260	265	270	
Met	Lys	Glu	Leu	Met	Glu	Leu	Ser	Glu	Pro	Glu	Arg	Ser	Ser	Arg	Trp	275	280	285	
Leu	Arg	Cys	Cys	Phe	Val	Glu	Asp	Leu	Glu	Cys	Glu	Ile	Thr	Gln	Ile	290	295	300	
Ala	Leu	Trp	Gln	Ala	Tyr	Gln	Ser	Arg	Phe	Ala	Asp	Pro	Arg	Leu	Pro	305	310	315	320

Gly Gly Gly Val Leu Pro Ala Ala Glu Phe Ile Lys Asn Val Ser Thr  
 325 330 335  
 Thr Phe Thr Asn Ala Gln Ala Gln Val Ile Asn Gly Pro Gly Ala Ala  
 340 345 350  
 Thr Lys Phe Ile Ile Lys Gly Ile Arg Pro Leu Glu Thr Ala Tyr Thr  
 355 360 365  
 Phe Glu Gly Phe Pro Tyr Ile Tyr Cys Lys Trp Ala Asp Asn Ser Lys  
 370 375 380  
 Pro Ser Lys Thr Cys Gln Arg Ala Phe Lys Ser Pro Ala Glu Leu Arg  
 385 390 395 400  
 His His Val Phe Thr Glu His Met Asn Leu Lys Pro Thr Glu Thr Pro  
 405 410 415  
 Gly His Tyr Asn Leu Glu Lys Ala Glu Ser Pro Val His Thr Cys Leu  
 420 425 430  
 Trp Asp Asn Cys Thr Lys Phe Arg Ser Ser Gly Pro Ser Ala Asn Thr  
 435 440 445  
 Ala Met Val Ala Gly His Val Ser Ala His Leu Pro Glu Glu Arg Ala  
 450 455 460  
 Pro Asp Ala Glu Pro Pro Thr Ser Lys Arg Ala Val Leu Gln Glu Arg  
 465 470 475 480  
 Ile Val Arg Lys Trp Tyr Tyr Leu Asp Thr Pro Val Asn Glu Arg Gly  
 485 490 495  
 Glu Pro Phe Gly Val Ala Tyr Lys Ala Ala Leu Val Leu Arg Asn Leu  
 500 505 510  
 Ala Arg Asn Leu Pro Thr Gly Ile Ala Pro Gln Tyr Asn Gly Leu Ser  
 515 520 525  
 Trp Lys Lys Ala Val Phe Leu Ser His Arg Pro Lys Ile Ile Glu Ala  
 530 535 540  
 Trp Asp Arg Asn Arg Ser Leu Arg Lys Glu Leu Thr Glu Leu Ile Met  
 545 550 555 560  
 Val Ile Glu Lys Glu Asp Tyr Tyr  
 565

<210> 143

<211> 2542

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA260; clone 2-10-21; contig 4849 region 12560-15101

Genomic sequence containing 3' and 5'-ends and the coding region

<400> 143

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aaaagcagat	actctcgtct	gctagaccgc	atactttgac	cggatcgggt	atcttccagt	180
acgagggtgc	tccgcatata	gtcacaattc	ctttttcaag	aggctttttc	ctcctctccc	240
tatccttttcg	ccctccctag	catccctttc	gagcttgcc	taatttcgtc	catctggcct	300
gtgtgccatt	ctcttcattg	cgatcaagg	ccttctctct	caggcggaca	cagccccct	360
gttcgtctgg	gcagcagata	gtgcttccta	ggcttctgtg	tctacgggtca	actacatata	420
caccactgcg	ttgctcctca	tctcaataat	cggctttgca	ccagcatacg	tcacacaatt	480
cattacgtca	atcagcggaa	atggtctaca	tccgcatccc	caagaactac	acggcttcgc	540
cgtcttcctt	tgccggaact	ccgtccttga	cgatcaatta	cgaggcaacg	caggatcttg	600
attctacca	tgcttttgaa	ggtttggtga	cgccgggtgac	acgtgtgaga	gcagcgtgg	660
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cttgtggtac	caccactctt	ctgtctggtc	tcccacgc	tctcgagatt	gccgctttgt	960
tccgtggctt	ccccagttct	accgcccctt	ctcgcggaat	ctccgtcgcc	gctgcgcct	1020
accgctctt	ctacagccgc	aagaacttcc	tggtccccga	ccgccagcgc	ggccctcacc	1080
gcagctggag	agatgaagtg	cggactatgg	ataagctctt	cctcaacggc	agcgcctaca	1140
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tcaccccgcc	aacgagcccc	ggagccaaga	ccgagtttac	ggaaacggag	accaaggctc	1260
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ttcgtgtaca	aagctcattg	actccctgta	ctgtcgttac	tgttctgatt	ttgcattgag	2280
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tcgtatgcga	atatttttta	taacatatat	ctaggatatg	tatccaagtt	caagaaggta	2400
gactcgtagt	agaatgtggt	gatccagttg	atggccgacg	ccaactggta	tcgattacgg	2460
attggcagac	gtgccagatc	agtcggaggt	ttcttttttg	ttgggatcgc	atcacagctc	2520
caacacgaca	ttcaactttc	aa				2542

&lt;210&gt; 144

&lt;211&gt; 1542

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA260; clone 2-10-21; contig 4849 region 12560-15101  
Genomic sequence containing the coding region

&lt;400&gt; 144

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cagcccgcgc	gtctgaaggc	tggtccggag	gagatctgga	aggacatggt	ggatctcgtc	300
aattgccagg	tccctcagat	tgtttcgtca	gaggatgtgg	acgcctacct	gctctccgag	360
tctagcatgt	tcgtttggcc	tcacaaactc	atcttgaaga	cttgtggtac	caccactctt	420
ctgtctggtc	tcccacgc	tctcgagatt	gccgctttgt	tccgtggctt	ccccagttct	480

accgccccctt	ctcgcggaat	ctccgtcgcc	gctgcgccct	accgcgcttt	ctacagccgc	540
aagaacttcc	tggtccccga	ccgccagcgg	ggccctcacc	gcagctggag	agatgaagtg	600
cggactatgg	ataagctctt	cctcaacggc	agcgccata	tgattggcaa	gatgaatggc	660
gagcactggg	acttgtaact	gactgaacct	cataccatgc	tcaccccgcc	aacgagcccg	720
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&lt;210&gt; 145

&lt;211&gt; 1482

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA260; clone 2-10-21; contig 4849 region 12560-15101  
Coding region without exons

&lt;400&gt; 145

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gggtccagaga	aactcttgga	ggtgtggttc	gcgccttcgc	ctcaggaatt	aggtccagcg	180
cagcccgccg	gtctgaaggc	tggtccggag	gagatctgga	aggacatggt	ggatctcgtc	240
aattgccagg	tcctctcgat	tgtttcgtca	gaggatgtgg	acgcctacct	gctctccgag	300
tctagcatgt	tcgtttggcc	tcacaaactc	atcttgaaga	cttgtggtac	caccactctt	360
ctgtctgggtc	tcccacgcat	tctcgagatt	gcccgtttgt	tcggtggctt	ccccaaagtct	420
accgccccctt	ctcgcggaat	ctccgtcgcc	gctgcgccct	accgcgcttt	ctacagccgc	480
aagaacttcc	tggtccccga	ccgccagcgg	ggccctcacc	gcagctggag	agatgaagtg	540
cggactatgg	ataagctctt	cctcaacggc	agcgccata	tgattggcaa	gatgaatggc	600
gagcactggg	acttgtaact	gactgaacct	cataccatgc	tcaccccgcc	aacgagcccg	660
ggagccaaga	ccgagtttac	ggaaacggag	accaaggtcc	tcagtgtacc	ccagggcgct	720
gctctgcaga	ctgattcggg	ggatgagact	ttggaagtct	tgatgaccga	cttggatgag	780
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gcgctcggaa	ccgtggtctc	tgaagcctgt	ggacttttct	ctgtgtatcc	taaggagaag	1020
tatcccgatt	cgcgcacga	tgccctacctg	tttacaccat	gcggcttctc	cgccaacggc	1080
gtgattccgc	ctcctgaggg	aaaagctgga	accactact	tcacagtaca	cgtcactcca	1140
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cggattgtcc	acgacctcga	cggctatgag	cttgtcttcc	gctattatga	acgcctggac	1440
tggaaagggg	gggcccctcg	gctgggagag	gagagatctt	ga		1482

&lt;210&gt; 146

&lt;211&gt; 493

&lt;212&gt; PRT

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA260; clone 2-10-21; contig 4849 region 12560-15101  
Protein sequence

&lt;400&gt; 146

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Met Val Tyr Ile Gly Ile Pro Lys Asn Tyr Thr Ala Ser Pro Ser Ser
1          5          10          15

Phe Ala Gly Thr Pro Ser Leu Thr Ile Asn Tyr Glu Ala Thr Gln Asp
          20          25          30

Leu Asp Ser Thr Asn Ala Phe Glu Gly Pro Glu Lys Leu Leu Glu Val
          35          40          45

Trp Phe Ala Pro Ser Ala Gln Glu Leu Gly Pro Ala Gln Pro Ala Gly
          50          55          60

Leu Lys Ala Val Pro Glu Glu Ile Trp Lys Asp Met Leu Asp Leu Val
65          70          75          80

Asn Cys Gln Val Leu Ser Ile Val Ser Ser Glu Asp Val Asp Ala Tyr
          85          90          95

Leu Leu Ser Glu Ser Ser Met Phe Val Trp Pro His Lys Leu Ile Leu
          100         105         110

Lys Thr Cys Gly Thr Thr Thr Leu Leu Ser Gly Leu Pro Arg Ile Leu
          115         120         125

Glu Ile Ala Ala Leu Phe Gly Gly Phe Pro Lys Ser Thr Ala Pro Ser
130         135         140

Arg Gly Ile Ser Val Ala Ala Ala Pro Tyr Arg Val Phe Tyr Ser Arg
145         150         155         160

Lys Asn Phe Leu Phe Pro Asp Arg Gln Arg Gly Pro His Arg Ser Trp
          165         170         175

Arg Asp Glu Val Arg Thr Met Asp Lys Leu Phe Leu Asn Gly Ser Ala
          180         185         190

Tyr Met Ile Gly Lys Met Asn Gly Glu His Trp Tyr Leu Tyr Leu Thr
195         200         205

Glu Pro His Thr Met Leu Thr Pro Pro Thr Ser Pro Gly Ala Lys Thr
210         215         220

Glu Phe Thr Glu Thr Glu Thr Lys Val Leu Ser Val Pro Gln Gly Ala
225         230         235         240

Ala Leu Gln Thr Asp Ser Glu Asp Glu Thr Leu Glu Val Leu Met Thr
          245         250         255

Asp Leu Asp Glu Glu Asn Ala Lys Gln Phe Tyr Leu Glu Asn Ala Thr
          260         265         270

Ala Val Ala Glu Asn Arg Tyr Arg Asn Ser Asn Ser Glu Lys Ser Gly
275         280         285

```

His Val Asp Val Phe Ser Asn Thr Ser Ser Asp Ile Ser Asp Phe Asp  
 290 295 300  
 Ser Asp Gly Ser Gln Val Leu Pro Pro Glu Leu Thr Thr Glu Gly His  
 305 310 315 320  
 Ala Leu Gly Thr Val Val Ser Glu Ala Cys Gly Leu Ser Ser Val Tyr  
 325 330 335  
 Pro Lys Glu Lys Tyr Pro Asp Ser Arg Ile Asp Ala Tyr Leu Phe Thr  
 340 345 350  
 Pro Cys Gly Phe Ser Ala Asn Gly Val Ile Pro Pro Pro Glu Gly Lys  
 355 360 365  
 Ala Gly Thr His Tyr Phe Thr Val His Val Thr Pro Glu Pro His Cys  
 370 375 380  
 Ser Tyr Ala Ser Phe Glu Thr Asn Val Pro His Ser Gln Asn Gly Gln  
 385 390 395 400  
 Thr Thr Ala Gly Ile Ile Lys Gln Val Val Asp Ile Phe Lys Pro Gly  
 405 410 415  
 Arg Phe Ser Val Thr Leu Phe Glu Ala Lys Pro Ala Leu Ser Gln Val  
 420 425 430  
 Glu Asp Glu Trp Lys Glu Ala Lys Tyr Leu Ala Ala Arg Arg Thr Ala  
 435 440 445  
 Lys Met Glu His Val Glu Gly Tyr Arg Arg Val Asp Arg Ile Val His  
 450 455 460  
 Asp Leu Asp Gly Tyr Glu Leu Val Phe Arg Tyr Tyr Glu Arg Leu Asp  
 465 470 475 480  
 Trp Lys Gly Gly Ala Pro Arg Leu Gly Glu Glu Arg Ser  
 485 490

<210> 147

<211> 1637

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA261; clone 7-5-9; contig 4857 region 164191-165827  
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 147

aaagatagag	aagacgttgc	gcggaacott	ttgaggaccc	tcagctctat	ttgagtgtct	60
gtcacgaggt	ccatatctgg	cgatacggag	ggctggctgt	acaattaggt	tactcttatt	120
tcctactgat	ctagtatat	aaagtttga	tgcattatgt	aaattaaatc	tcgggggcaa	180
atgaacattt	cgaatatcgt	tataaaactc	acagaaagtg	ctgtcaatgg	cacaaattta	240
gcaatcaata	ctcatctgag	tatgttgttg	ataagtcgga	aaacaaccta	aatatattacc	300
tcattaggaa	aggtgcactc	cgtagttacc	tcgactcgcg	gttagtctgg	tgactaagtt	360
cttggcgttg	tgatgagggc	aagtcctatc	atgtgatcat	agttagggtt	tccacacacc	420
aggctctcca	atatagcaag	aaaatagaag	gattaggtct	cgtctccgaa	catccatccc	480
gccagcacac	aaccgccaaa	atgggtcgcg	ttagaaccaa	ggtaagttac	agatgaagca	540
tcatgagtta	tcttcaaaaa	agcccaaaaa	gagtatcatt	tctgacgaaa	tgggtttttc	600
ttcaatagac	agtcaagagg	tccgccaagg	tcatcatcga	gcgctactac	cccaagttga	660

cgctcgactt	tgagaccaac	aagcgtcttt	gcgatgagat	cgctatcatt	gcctccaagc	720
gccttcgcaa	caaggtgggc	aatccatcac	tgagccgtac	aacagtcgga	atttgacttg	780
ctgacgaaaa	ctagattgct	ggttacacca	cccaccttat	gaagcgtatc	cagcgtggcc	840
ctgtccgcgg	tatctctttc	aagctgcagg	aggaggagcg	tgagcgcaag	gatcagtacg	900
ttcctgaggt	ttccgctctg	gatgtttccc	agaccgagtc	cggccagctc	gatgtcgatg	960
ccgacaccaa	ggaccttctc	aagtccatgg	gcgtaagttc	tgttctcaac	gcggttggtc	1020
gtggttttaa	agcagtcctg	taacttatat	tgcccactac	agttcgacaa	tctcaaggtc	1080
aacgttgtca	acgtctccca	acatcagggt	caggagcgcc	cccgccgctt	ccggtagatg	1140
cgcgcacccc	tcgagcctcg	aaaaaaaaag	taccgattgt	cttcggtcga	tctatggcgt	1200
gctcaatcac	acttgctctg	gctgacttcg	cagctatgat	gtagcctaga	gacacaggaa	1260
tgaacataat	tctctctgag	aaaggtgtcg	ctgattctcc	tgggtggagat	gacgcttgat	1320
tgccaaaatt	tctccttttg	cttactgtcc	gtttcagctc	gggcgctgcg	tagaagggtc	1380
tctctgcatg	atgcgcagga	tgtcatcaga	gagtcgaaac	ctttggtgcg	aactgcacca	1440
tcaactgcac	cgcattggat	cagatccata	ttaatcagtc	tatctacaga	agtaaattgg	1500
gtatcgatcat	aagcacaaag	acgccgtaga	accacaaatc	gaaccacccc	atcgaattct	1560
gtcgtgacca	ggctcacgcc	aaaccgcgtg	agattgaagc	atatcatgat	cagatttcct	1620
ttggcacgta	gccttca					1637

&lt;210&gt; 148

&lt;211&gt; 637

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA261; clone 7-5-9; contig 4857 region 164191-165827  
Genomic sequence containing the coding region

&lt;400&gt; 148

atgggtcgcg	ttagaaccaa	ggtaagttac	agatgaagca	tcatgagtta	tcttcaaaaa	60
agcccaaaa	gagtatcatt	tctgacgaaa	tgggtttttc	ttcaatagac	agtcaagagg	120
tccgccaaag	tcatcatcga	gcgctactac	cccaagttga	cgctcgactt	tgagaccaac	180
aagcgtcttt	gcgatgagat	cgctatcatt	gcctccaagc	gccttcgcaa	caaggtgggc	240
aatccatcac	tgagccgtac	aacagtcgga	atttgacttg	ctgacgaaaa	ctagattgct	300
ggttacacca	cccaccttat	gaagcgtatc	cagcgtggcc	ctgtccgcgg	tatctctttc	360
aagctgcagg	aggaggagcg	tgagcgcaag	gatcagtacg	ttcctgaggt	ttccgctctg	420
gatgtttccc	agaccgagtc	cggccagctc	gatgtcgatg	ccgacaccaa	ggaccttctc	480
aagtccatgg	gcgtaagttc	tgttctcaac	gcggttggtc	gtggttttaa	agcagtcctg	540
taacttatat	tgcccactac	agttcgacaa	tctcaaggtc	aacgttgtca	acgtctccca	600
acatcagggt	caggagcgcc	cccgccgctt	ccggtag			637

&lt;210&gt; 149

&lt;211&gt; 420

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA261; clone 7-5-9; contig 4857 region 164191-165827  
Coding region without exons

&lt;400&gt; 149

atgggtcgcg	ttagaaccaa	gacagtcaag	aggcccgcca	aggatcatcat	cgagcgctac	60
taccccaagt	tgacgctcga	ctttgagacc	aacaagcgtc	tttgcgatga	gatcgctatc	120
attgcctcca	agcgccttcg	caacaagatt	gctggttaca	ccaccacct	tatgaagcgt	180
atccagcgtg	gccctgtccg	cggatatctc	ttcaagctgc	aggaggagga	gcgtgagcgc	240
aaggatcagt	acgttccctga	ggtttccgct	ctggatgttt	cccagaccga	gtccggccag	300
ctcgatgtcg	atgccgacac	caaggacctt	ctcaagtcca	tgggcttcga	caatctcaag	360
gtcaacggtt	tcaacgtctc	ccaacatcag	gttcaggagc	gccccgcgcg	cttcgggtag	420

&lt;210&gt; 150



<211> 139  
 <212> PRT  
 <213> *Aspergillus fumigatus*

<220>  
 <223> Phylum CEA261; clone 7-5-9; contig 4857 region 164191-165827  
 Protein sequence

<400> 150

```

Met Gly Arg Val Arg Thr Lys Thr Val Lys Arg Ser Ala Lys Val Ile
1          5          10          15
Ile Glu Arg Tyr Tyr Pro Lys Leu Thr Leu Asp Phe Glu Thr Asn Lys
          20          25          30
Arg Leu Cys Asp Glu Ile Ala Ile Ile Ala Ser Lys Arg Leu Arg Asn
          35          40          45
Lys Ile Ala Gly Tyr Thr Thr His Leu Met Lys Arg Ile Gln Arg Gly
          50          55          60
Pro Val Arg Gly Ile Ser Phe Lys Leu Gln Glu Glu Glu Arg Glu Arg
65          70          75          80
Lys Asp Gln Tyr Val Pro Glu Val Ser Ala Leu Asp Val Ser Gln Thr
          85          90          95
Glu Ser Gly Gln Leu Asp Val Asp Ala Asp Thr Lys Asp Leu Leu Lys
          100          105          110
Ser Met Gly Phe Asp Asn Leu Lys Val Asn Val Val Asn Val Ser Gln
          115          120          125
His Gln Val Gln Glu Arg Pro Arg Arg Phe Arg
          130          135

```

<210> 151  
 <211> 2037  
 <212> DNA  
 <213> *Aspergillus fumigatus*

<220>  
 <223> Phylum CEA262; clone 10-2-18  
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 151

```

aaggtagtag gtgcagatat tgttgataga catttcaaaa tgtattagtt acatgattac      60
ttacttagat gtaatctttc gataataactt tctagtcttg ttgagttcag aaggccagtg      120
tgtgctgaaa atgacagcga cctatgcggt gcccggtgag cgaagagcac tggctggaaa      180
taagaagttt attagaggag cctcatgatg cataatcatt gtaagcgcac gatgcacaat      240
aatatatccg aatttctcca gatgacacta agataataac gaaaatatca catgacgttg      300
tgggcaggta tgtattatgt aatctgatcg gtagggccga tgtctcgctt agcggacttt      360
tctgtgggat tgcaatttca acttattatt ccgccgacca gcaacaaagc gggtactcga      420
ctcgactccc tccaccagag cccgtggtgt gatataacctg tctgtctttg atcctcgcaa      480
gatagacttg agtcgcagtt atggcggttg gaaagtatgc caattcactt ctattattgt      540
tctgaacgct tttagcatgt gtctggatac ggtggtttac aggtactgat ccggaacag      600
gaacaagcgc ttgtcgaagg gcaagaaggg tgtaagaag aggaccgttg atcctttctc      660
caggaaggac gaataactctg ttaaggatatg tcgacgtgga ctgtgtaagt cgaccgcagc      720
taatctatat caggcgcctt ccactttcca gatcagagag tatgttgcac gcatatgatg      780

```

tcgaattgca	ggataaaggc	gattcacaaat	ggtagtggag	attatgctga	ctgaattata	840
gtgtcgggaa	gactctggtc	aaccgcacca	gtggtctcaa	gaacgccaat	gactccctga	900
agggtcgaat	tttcgaggtc	tcgctggctg	acctgcagaa	tgatgaagac	catgctttcc	960
gcaagggttaa	gcttcgtgtg	gacgaggttc	agggcaagaa	ctgtttgacc	aacttccacg	1020
gtcttgattt	cacaaccgac	aaattgcat	ccctcgtgcg	caagtggcag	tcgctgatcg	1080
aagccaatgt	cactgtgaag	acgaccgatg	attatctcct	tcggcttttt	gctatcgctt	1140
tcaccaagag	acgcccgaac	cagattaaga	agaccacata	tgctcgttct	tctcaaatacc	1200
gtgccatccg	caagaagatg	attgaaatca	tgacagagga	ggcagccagc	tgctctctcg	1260
ctcagctcac	tcacaagctc	attcctgagg	tcattgggtcg	tgagatcgag	aaggctaccc	1320
agggaaatcta	tcctttgacg	aatgtgtgtg	accctgttat	tcttactcgg	gatgaagact	1380
aactgcaatc	taggtccata	ttcgcaaggt	caagcttctt	aaggctccca	agttcgacct	1440
gggtgcactg	ctgaatctgc	acggtgaatc	tacaaccgat	gataagggcc	acaaggtcga	1500
gagagagttc	aaggagcagg	ttctcgaaag	cgtttaagtg	gactgaatta	ccagtatgct	1560
ggttatttcgg	gacattgatt	tgtacctacc	tgtatgcttg	gattcttttt	ttatgagtta	1620
aaatgggaaa	agaacttttg	tcgcggcatc	atgtctttat	tgactgggtg	tgctgttaac	1680
ttctatgtcc	tttgagaatg	gagcttgcaa	agaaaacttt	gcccttattc	aaatatttaa	1740
ttggacaatt	ccgatcaaag	tttagcagta	gaatacctgc	tataccagtg	atgtgctgat	1800
gcaacgggca	cctgcagttt	actttcagtt	gattcaaatt	ctatattaac	agagcccttt	1860
taccacacca	ctgacctggt	attagtatag	tgtctcgccc	taggagacta	aagaattgct	1920
agaagtatgg	ttatacataa	tgttgaaatg	ttagtatgat	ttattaatat	tattttcagt	1980
gcactgatat	atatcataat	gctactaaat	atagctaccc	taagatttat	atagaga	2037

&lt;210&gt; 152

&lt;211&gt; 1037

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

&lt;223&gt; Phylum CEA262; clone 10-2-18

Genomic sequence containing the coding region

&lt;400&gt; 152

atggcggttg	gaaagtatgc	caattcactt	ctattattgt	tctgaacgct	tttagcatgt	60
gtctggatac	ggtggtttac	aggtactgat	ccgggaacag	gaacaagcgc	ttgtcgaagg	120
gcaagaaggg	tgtaagaag	aggaccgttg	atcctttctc	caggaaggac	gaataactctg	180
ttaagggtatg	tcgacgtgga	ctgtgttaagt	cgaccgcagc	taatctatat	caggcgctt	240
ccactttcca	gatcagagag	tatgtttgcac	gcataatgatg	tcgaattgca	ggataaaggc	300
gattcacaaat	ggtagtggag	attatgctga	ctgaattata	gtgtcgggaa	gactctggtc	360
aaccgcacca	gtggtctcaa	gaacgccaat	gactccctga	agggtcgaat	tttcgaggtc	420
tcgctggctg	acctgcagaa	tgatgaagac	catgctttcc	gcaagggttaa	gcttcgtgtg	480
gacgaggttc	agggcaagaa	ctgtttgacc	aacttccacg	gtcttgattt	cacaaccgac	540
aaattgcat	ccctcgtgcg	caagtggcag	tcgctgatcg	aagccaatgt	cactgtgaag	600
acgaccgatg	attatctcct	tcggcttttt	gctatcgctt	tcaccaagag	acgcccgaac	660
cagattaaga	agaccacata	tgctcgttct	tctcaaatacc	gtgccatccg	caagaagatg	720
attgaaatca	tgacagagga	ggcagccagc	tgctctctcg	ctcagctcac	tcacaagctc	780
attcctgagg	tcattgggtcg	tgagatcgag	aaggctaccc	agggaaatcta	tcctttgacg	840
aatgtgtgtg	accctgttat	tcttactcgg	gatgaagact	aactgcaatc	taggtccata	900
ttcgcaaggt	caagcttctt	aaggctccca	agttcgacct	gggtgcactg	ctgaatctgc	960
acggtgaatc	tacaaccgat	gataagggcc	acaaggtcga	gagagagttc	aaggagcagg	1020
ttctcgaaaag	cgtttaa					1037

&lt;210&gt; 153

&lt;211&gt; 771

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

&lt;223&gt; Phylum CEA262; clone 10-2-18

Coding region without exons

```

<400> 153
atggcggttg gaaagaacaa gcgcttgctg aagggcaaga aggggtgttaa gaagaggacc      60
gttgatcctt tctccaggaa ggacgaatac tctgttaagg cgccttccac tttccagatc      120
agagatgtcg ggaagactct ggtcaaccgc accagtggtc tcaagaacgc caatgactcc      180
ctgaagggtc gaattttcga ggtctcgtcg gctgacctgc agaatgatga agaccatgct      240
ttccgcaagg ttaagcttcg tgtggacgag gttcagggca agaactgttt gaccaacttc      300
cacggtcttg atttcacaac cgacaaattg cgatccctcg tgcgcaagtg gcagtcgctg      360
atcgaagcca atgtcactgt gaagacgacc gatgattatc tccttcggct ttttgctatc      420
gccttcacca agagacgccc gaaccagatt aagaagacca catatgctcg ttcttctcaa      480
atccgtgcca tccgcaagaa gatgattgaa atcatgcaga gggaggcagc cagctgctct      540
ctcgctcagc tcaactacaa gctcattcct gaggtcattg gtcgtgagat cgagaaggct      600
ccccagggaa tctatccttt gcagaatgtc catattcgca aggtcaagct tcttaaggct      660
cccaagttcg acctgggtgc actgctgaat ctgcacggtg aatctacaac cgatgataag      720
ggccacaagg tcgagagaga gttcaaggag caggttctcg aaagcgttta a              771

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<210> 154

<211> 256

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA262; clone 10-2-18  
Protein sequence

<400> 154

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Met Ala Val Gly Lys Asn Lys Arg Leu Ser Lys Gly Lys Lys Gly Val
1              5              10              15

Lys Lys Arg Thr Val Asp Pro Phe Ser Arg Lys Asp Glu Tyr Ser Val
20              25              30

Lys Ala Pro Ser Thr Phe Gln Ile Arg Asp Val Gly Lys Thr Leu Val
35              40              45

Asn Arg Thr Ser Gly Leu Lys Asn Ala Asn Asp Ser Leu Lys Gly Arg
50              55              60

Ile Phe Glu Val Ser Leu Ala Asp Leu Gln Asn Asp Glu Asp His Ala
65              70              75              80

Phe Arg Lys Val Lys Leu Arg Val Asp Glu Val Gln Gly Lys Asn Cys
85              90              95

Leu Thr Asn Phe His Gly Leu Asp Phe Thr Thr Asp Lys Leu Arg Ser
100             105             110

Leu Val Arg Lys Trp Gln Ser Leu Ile Glu Ala Asn Val Thr Val Lys
115             120             125

Thr Thr Asp Asp Tyr Leu Leu Arg Leu Phe Ala Ile Ala Phe Thr Lys
130             135             140

Arg Arg Pro Asn Gln Ile Lys Lys Thr Thr Tyr Ala Arg Ser Ser Gln
145             150             155             160

Ile Arg Ala Ile Arg Lys Lys Met Ile Glu Ile Met Gln Arg Glu Ala
165             170             175

```

Ala Ser Cys Ser Leu Ala Gln Leu Thr His Lys Leu Ile Pro Glu Val  
 180 185 190  
 Ile Gly Arg Glu Ile Glu Lys Ala Thr Gln Gly Ile Tyr Pro Leu Gln  
 195 200 205  
 Asn Val His Ile Arg Lys Val Lys Leu Leu Lys Ala Pro Lys Phe Asp  
 210 215 220  
 Leu Gly Ala Leu Leu Asn Leu His Gly Glu Ser Thr Thr Asp Asp Lys  
 225 230 235 240  
 Gly His Lys Val Glu Arg Glu Phe Lys Glu Gln Val Leu Glu Ser Val  
 245 250 255

<210> 155

<211> 1819

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA263; clone 4-3-3; contig 4944 region 159432-161250  
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 155

aattcatcag	cataacgaac	ccccaacgac	ttcgaaaaaa	aagcccgatt	cgaaagaatt	60
gcgcattcaa	cataccatgg	tgggcggcct	cgtgtcgtgt	cgtacgggta	ttgtcgacaa	120
tgaggattga	agatgggcca	ggtcaatttg	ggatgttcgt	tgtgggacta	gggttttttt	180
ctgtgttggt	gcggtcacgc	tgcggctggg	ctaagcgggc	acgtgactgt	ggctgactgc	240
ctggtgacgc	cccccccgg	aggaaccccc	aaccggcagc	cagataggct	cgggaggatc	300
atcgctgaat	gatggcattg	ttcttggctt	cagtggatgg	gttattaatg	actgcctgga	360
cggctggatg	actccgtcgc	tgatttagca	ttgtgatcca	cgatttatgt	ttcattttctg	420
gggcgcgggt	ttactaccat	cacttttgtc	actaccatca	cttttatact	gagttttctga	480
ccccgacccc	gaaccagact	atggcaactt	cgactgggac	cggatgggct	cagctccggc	540
agcaagcccg	ttcgcttgag	actcaggtac	ggaactcgaa	actacgctat	aatgaggcct	600
tactcgtgat	ttggatgttg	acaataatgt	tcctagaccg	agagtctgtt	tcacacctat	660
gcgcagtatg	catcgatgac	gaagctgcct	ccgaaaccct	cagaagaaga	acaacggatt	720
gaatcgcaac	tgaaggatct	tcttgaaaag	gtgtgcactt	tgaggccctc	tagtccagcc	780
caacagacga	tcatgctgac	acgatccgat	catagcgtga	agccctcatc	tcccagctct	840
cccgctcctt	tgactccgaa	gccactctta	ccgcactctgc	cctgaaacag	agcaatcttg	900
cccgcaatcg	cgaagtcctc	caggatcatc	gccgcgaatt	gcagcgcctg	aacgcgcgaa	960
tcgccgagtc	ccgcgaccga	gccaatcttc	tgtctaactg	ccgctccgac	attgatgcct	1020
accgcaattc	aaaccccggc	gcggctgagg	cagactacat	gctcgaggag	cggggctgta	1080
tagatgaaag	ccataacatg	atagatggtg	tcctaagcca	ggcgtatgca	atcaacgaga	1140
gttttgggct	acaacgtgaa	accctggcca	gcatcaatcg	ccgtatcgtc	ggtgctgcca	1200
ataaggtacc	aggaatgaat	gcattgattg	gtaagattgg	gacgaagagg	agacgtgacg	1260
caatcatctt	gggggctttc	atcggtcttt	gtttcttgat	ggtgttcttc	ttccgatgag	1320
atgctggtgc	tccgtatacc	gccgatcttc	ctgtgttata	attccttgct	caacggtatc	1380
tacatcggag	accgcacggc	gttcgggtgt	tttcatgtac	tccttttctg	catgcaagca	1440
ctaatacaca	tggtcatggc	gtttcagggt	gtctatttca	catttatgta	catacagggt	1500
cagactgctg	tagccctagg	gctcaccgca	tgatcactct	tggttttcgga	cttgccgatt	1560
caccttggtt	tcttcccggc	cattcctcag	ccggtagctt	cgactcgaga	ctgattcttc	1620
tctcctggat	taattttgca	accccgttgt	tcaatccgtc	tagctcgccct	tcctctgccg	1680
gcccgcctacc	cgcccatcgg	atgcgacagt	tctcgtccag	cagatagaca	taaccaactt	1740
tactgttcat	cattccgatt	gcttctttca	acccatccgt	aagacctttg	cgcacaagga	1800
aataccgttc	gtgctgctc					1819

<210> 156

<211> 819

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA263; clone 4-3-3; contig 4944 region 159432-161250  
Genomic sequence containing the coding region

<400> 156

atggcaactt	cgactgggac	cggatgggct	cagctccggc	agcaagcccg	ttcgcttgag	60
actcaggtac	ggaactcgaa	actacgctat	aatgaggctt	tactcgtgat	ttggatgttg	120
acaataatgt	tcctagaccg	agagtctgtt	tcacacctat	gcgcagtatg	catcgatgac	180
gaagctgcct	ccgaaaccct	cagaagaaga	acaacggatt	gaatcgcaac	tgaaggatct	240
tcttgaaaag	gtgtgcaact	tgaggccctc	tagtccagcc	caacagacga	tcattgctgac	300
acgatccgat	catagcgtga	agccctcatc	tcccagctct	cccgtctcct	tgactccgaa	360
gccactctta	ccgcatctgc	cctgaaacag	agcaatcttg	cccgcgaatcg	cgaagtcctc	420
caggatcatc	gccgcgaatt	gcagcgcctg	aacgcgcgaa	tcgccgagtc	ccgcgaccga	480
gccaatcttc	tgtctaactg	ccgctccgac	attgatgcct	accgcaattc	aaaccccgcc	540
gcggctgagg	cagactacat	gctcgaggag	cggggtcgta	tagatgaaag	ccataacatg	600
atagatgggtg	tcctaagcca	ggcgtatgca	atcaacgaga	gttttgggct	acaacgtgaa	660
accctggcca	gcatcaatcg	ccgtatcgtc	ggtgctgcca	ataaggtacc	aggaatgaat	720
gcattgattg	gtaagattgg	gacgaagagg	agacgtgacg	caatcatctt	gggggctttc	780
atcggctttt	gtttcttgat	ggtgttcttc	ttccgatga			819

<210> 157

<211> 684

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA263; clone 4-3-3; contig 4944 region 159432-161250  
Coding region without exons

<400> 157

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ccgaaaccct	cagaagaaga	acaacggatt	gaatcgcaac	tgaaggatct	tcttgaaaag	180
cgtgaagccc	tcattctccc	gctctcccg	ctccttgact	ccgaagccac	tcttaccgca	240
tctgccctga	aacagagcaa	tcttgcccgc	aatcgcgaa	tcctccagga	tcattcgccgc	300
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aacgtccgct	ccgacattga	tgcctaccgc	aattcaaacc	ccgccgcggc	tgaggcagac	420
tacatgctcg	aggagcgggg	tcgtatagat	gaaagccata	acatgataga	tggtgtccta	480
agccaggcgt	atgcaatcaa	cgagagtttt	gggctacaac	gtgaaaccct	ggccagcatc	540
aatcgccgta	tcgtcgggtc	tgccaataag	gtaccaggaa	tgaatgcatt	gattggtaag	600
attgggacga	agaggagacg	tgacgcaatc	atcttggggg	ctttcatcgc	cttttgtttc	660
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<210> 158

<211> 227

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA263; clone 4-3-3; contig 4944 region 159432-161250  
Protein sequence

<400> 158

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                   20                                  25                                  30  
 Tyr Ala Ser Met Thr Lys Leu Pro Pro Lys Pro Ser Glu Glu Glu Gln  
                   35                                  40                                  45  
 Arg Ile Glu Ser Gln Leu Lys Asp Leu Leu Glu Lys Arg Glu Ala Leu  
                   50                                  55                                  60  
 Ile Ser Gln Leu Ser Arg Leu Leu Asp Ser Glu Ala Thr Leu Thr Ala  
                   65                                  70                                  75                                  80  
 Ser Ala Leu Lys Gln Ser Asn Leu Ala Arg Asn Arg Glu Val Leu Gln  
                   85                                  90                                  95  
 Asp His Arg Arg Glu Leu Gln Arg Leu Asn Ala Ala Ile Ala Glu Ser  
                   100                                  105                                  110  
 Arg Asp Arg Ala Asn Leu Leu Ser Asn Val Arg Ser Asp Ile Asp Ala  
                   115                                  120                                  125  
 Tyr Arg Asn Ser Asn Pro Ala Ala Ala Glu Ala Asp Tyr Met Leu Glu  
                   130                                  135                                  140  
 Glu Arg Gly Arg Ile Asp Glu Ser His Asn Met Ile Asp Gly Val Leu  
                   145                                  150                                  155                                  160  
 Ser Gln Ala Tyr Ala Ile Asn Glu Ser Phe Gly Leu Gln Arg Glu Thr  
                   165                                  170                                  175  
 Leu Ala Ser Ile Asn Arg Arg Ile Val Gly Ala Ala Asn Lys Val Pro  
                   180                                  185                                  190  
 Gly Met Asn Ala Leu Ile Gly Lys Ile Gly Thr Lys Arg Arg Arg Asp  
                   195                                  200                                  205  
 Ala Ile Ile Leu Gly Ala Phe Ile Gly Phe Cys Phe Leu Met Val Phe  
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 Phe Phe Arg  
 225

&lt;210&gt; 159

&lt;211&gt; 2601

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

&lt;223&gt; Phylum CEA264; contig 4899 region 65039-62439

Genomic sequence containing 3' and 5'-ends and the coding region

&lt;400&gt; 159

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ttactgtttt	cccaaacgaa	tccattatta	tttctttccc	ttggagggtc	cctactgtgg	180
tcttggtgtc	gcactcttgc	caagcccat	ggtccttgct	ctgagcctat	cacttgcgat	240
tcgcccgcgc	ataagtccgc	ctctctcaac	ctttccatct	cacgcgcacc	tccactcaac	300
atccaccatt	cggatattcc	gcccattcaa	agcgaacacc	cctccttctg	ctccaccatc	360
gattgcagtc	tgcccaaaac	ggacttcaga	actcccttct	acgctathtt	ccgccattca	420
ctggttgaagt	gcagccctcc	atactctcga	tagcaactgc	ccaaccccc	tcttactgcc	480

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ctgtggaact aactgctttg ctttccgacc atacagaagt cgtccgcgag aaggtccagg 660
atggactgac aggggaaaact aaggagattt cgtactcaca atgtaaaatc gtcggcaatg 720
gatcgttttg tgtcgtcttt cagacgaaaa tgatgccaaag cggcgaggat gctgccatta 780
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gcggattgtt cgccatccta acatcgtaga attgaaagcc ttctattact cgaacggcga 960
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tccttgaga gtcgggaatt gaccaactgg tggaaatcat caaggttctt ggaacccta 1560
ctcgggagca gatccgcacc atgaacccaa actatatgga gcacaaattc cctcaaatca 1620
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gtcatagtct ggagttttcg aggtgtctga gacagctctt gggaaaggaa aaaaagtgat 2520
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gaaggaggac atgaccattc c 2601

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<210> 160

<211> 1601

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA264; contig 4899 region 65039-62439

Genomic sequence containing the coding region

<400> 160

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ctttccgacc atacagaagt cgtccgcgag aaggtccagg atggactgac aggggaaact 180
aaggagattt cgtactcaca atgtaaaatc gtcggcaatg gatcgttttg tgtcgtcttt 240
cagacgaaaa tgatgccaaag cggcgaggat gctgccatta agagggtcct tcaagacaag 300
cgcttcaaag tatgtgtaca ttataagggc aattgccctc gctgcccac ccaaagatac 360
tgtcgtgac gagataccag aatcgagaac tgcagattat gcggattgtt cgccatccta 420
acatcgtaga attgaaagcc ttctattact cgaacggcga gagggtatgc gactctcctt 480
tgtctcccca ttcgttctag tttgccgttt gctgactacc ctaccattgt ctttcacaga 540
aggatgaagt gtacctaaac ctcgttctcg aatacgtaac agaaaccgtg tatcgggcgt 600
cgcggtactt taataaactc aaaacgacta tgccaatgtt ggaagtcaag ctgtatatct 660
atcaattgtt ccgttccctg gcatacatcc attcacaagg catctgccac cgtgacatca 720
agccccagaa tctcttactt gatccatcca ccggcatcct caaactctgc gactttggtt 780

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cggccaaagat tctggtagag aatgagccca acgttttcta tatctgttcc cgctactatc 840
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tgattcctcc ttcaagtttg gtactgtcat gctgacgac gtcaagacgt gtggtccacg 960
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gcttattcgc tgatcactct tttgtagaac tttctattgc acctgcattg aacagccggc 1500
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ctcctctcac gaaggaggag atgatggcac gtctcgactg a 1601

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<210> 161

<211> 1185

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA264; contig 4899 region 65039-62439

Coding region without exons

<400> 161

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gtcggcaatg gatcggttgg tgtcgtcttt cagacgaaaa tgatgccaag cggcgaggat 180
gctgccatta agagggctct tcaagacaag cgcttcaaaa atcgagaact gcagattatg 240
cggattgttc gccatcctaa catcgtagaa ttgaaagcct tctattactc gaacggcgag 300
aggaaaggatg aagtgtacct aaacctcggt ctogaatacg taccagaaac cgtgtatcgg 360
gcgtcgcgggt actttaataa actcaaaacg actatgccaa tgttggaagt caagctgtat 420
atctatcaat tgttccgttc cctggcatac atccattcac aaggcatctg ccaccgtgac 480
atcaagcccc agaattctctt acttgatcca tccaccggca tcctcaaact ctgcgacttt 540
ggttcggcca agattctggt agagaatgag cccaacgttt cctatatctg ttcccgtac 600
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tccacgggtt gtgtgatggc tgaactcatg cttggtcagc cattgttccc tggagagtcg 720
ggaattgacc aactggtgga aatcatcaag gttcttgga cccctactcg ggagcagatc 780
cgcaccatga acccaaacta tatggagcac aaattccctc aaatcaagcc acaccattc 840
aacaaggttt tccggagagc tcctcacgag gccattgatc tgatctcagc tttgctagaa 900
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cggctggttc cccctcatgc acgcgcogct ctcgaggccc gggggctaga cattgacaac 1140
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<210> 162

<211> 394

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA264; contig 4899 region 65039-62439

Protein sequence

<400> 162

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1           5           10           15

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 Ile Ser Tyr Ser Gln Cys Lys Ile Val Gly Asn Gly Ser Phe Gly Val  
 35 40 45  
 Val Phe Gln Thr Lys Met Met Pro Ser Gly Glu Asp Ala Ala Ile Lys  
 50 55 60  
 Arg Val Leu Gln Asp Lys Arg Phe Lys Asn Arg Glu Leu Gln Ile Met  
 65 70 75 80  
 Arg Ile Val Arg His Pro Asn Ile Val Glu Leu Lys Ala Phe Tyr Tyr  
 85 90 95  
 Ser Asn Gly Glu Arg Lys Asp Glu Val Tyr Leu Asn Leu Val Leu Glu  
 100 105 110  
 Tyr Val Pro Glu Thr Val Tyr Arg Ala Ser Arg Tyr Phe Asn Lys Leu  
 115 120 125  
 Lys Thr Thr Met Pro Met Leu Glu Val Lys Leu Tyr Ile Tyr Gln Leu  
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 Phe Arg Ser Leu Ala Tyr Ile His Ser Gln Gly Ile Cys His Arg Asp  
 145 150 155 160  
 Ile Lys Pro Gln Asn Leu Leu Leu Asp Pro Ser Thr Gly Ile Leu Lys  
 165 170 175  
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 180 185 190  
 Val Ser Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala Pro Glu Leu Ile Phe  
 195 200 205  
 Gly Ala Thr Asn Tyr Thr Thr Lys Ile Asp Val Trp Ser Thr Gly Cys  
 210 215 220  
 Val Met Ala Glu Leu Met Leu Gly Gln Pro Leu Phe Pro Gly Glu Ser  
 225 230 235 240  
 Gly Ile Asp Gln Leu Val Glu Ile Ile Lys Val Leu Gly Thr Pro Thr  
 245 250 255  
 Arg Glu Gln Ile Arg Thr Met Asn Pro Asn Tyr Met Glu His Lys Phe  
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 Pro Gln Ile Lys Pro His Pro Phe Asn Lys Val Phe Arg Arg Ala Pro  
 275 280 285  
 His Glu Ala Ile Asp Leu Ile Ser Ala Leu Leu Glu Tyr Thr Pro Thr  
 290 295 300  
 Gln Arg Leu Ser Ala Ile Glu Ala Met Cys His Pro Phe Phe Asp Glu  
 305 310 315 320  
 Leu Arg Asp Pro Asn Thr Arg Leu Pro Asp Ser Arg His Pro Gly Gly  
 325 330 335

Ala Ala Arg Asp Leu Pro Asn Leu Phe Asp Phe Ser Arg His Glu Leu  
340 345 350

Ser Ile Ala Pro Ala Leu Asn Ser Arg Leu Val Pro Pro His Ala Arg  
355 360 365

Ala Ala Leu Glu Ala Arg Gly Leu Asp Ile Asp Asn Phe Thr Pro Leu  
370 375 380

Thr Lys Glu Glu Met Met Ala Arg Leu Asp  
385 390

<210> 163

<211> 2539

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA265; clone 11-4-9; contig 4826 region 355652-358190  
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 163

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gcgctgtggc	atggcgatcc	gatcaggagg	atgatgacat	cgtggacagg	ttgtgggaga	180
gcggacgaga	taggacggag	aacgggttga	agaggggtcaa	taacgaccct	ttgaagcgta	240
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ctgtcgcagt	tcgcagcttc	ttctcctcat	ctcggtgcg	ggctggcatt	gccgatcatg	660
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catactagac	tgcttttttg	gcatgggagg	ctggcgctcg	tgtataacaa	attcttttta	2160
aacttcactc	atgatgatcc	gcaacacgta	gatatagctt	caacatgaat	tgattcaggt	2220
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tttaaacgaa	gatggtaggt	ttctaattgct	tctttcgtca	tcattgctagg	agccttgacc	2520
atggcatcat	cgccaccct					2539

&lt;210&gt; 164

&lt;211&gt; 1539

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA265; clone 11-4-9; contig 4826 region 355652-358190  
Genomic sequence containing the coding region

&lt;400&gt; 164

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gagtcgatta	cttcacagtc	tacttcacaa	gagttacctc	atcgccggag	gaagcggtta	360
aaggaagagg	cggccaagaa	taatgctgca	gaaaccgaac	tccctcctga	tgctcgtct	420
caattgtcca	ccctctcatc	agccctccct	gcgacttccc	tgccgcgcaa	gctggctgcg	480
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tatgggatgt	accgatctc	ctctcttctc	acacttgacc	cttcaatgac	tccctaccg	600
accctctcga	cctcaacctt	gacctttctc	tacctgacca	caggaacctt	cttgtcttca	660
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&lt;210&gt; 165

&lt;211&gt; 1539

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA265; clone 11-4-9; contig 4826 region 355652-358190  
Coding region without exons

&lt;400&gt; 165

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gtcaatagct	cccctcgaag	tattgccgac	aatgcgttat	cacaggggtgc	agccagttcg	300
gagtcgatta	cttcacagtc	tacttcacaa	gagttacctc	atcgccggag	gaagcggtta	360

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tttctcgccc tcacaaagcc tcgtctctcg ttccctgacgac tacctccgct 540
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<210> 166

<211> 512

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA265; clone 11-4-9; contig 4826 region 355652-358190  
Protein sequence

<400> 166

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Arg Pro Val Ala Val Arg Ser Phe Phe Ser Ser Ser Arg Leu Arg Ala
          35           40           45

Gly Ile Ala Asp His Glu Ser Thr Pro Ser Thr Val Gln Lys Thr Tyr
50           55           60

Phe Ser Ala Asn Arg Thr Ala Asp Gly Leu Leu Ala Ser Leu Ser Ala
65           70           75           80

Val Asn Ser Ser Pro Arg Ser Ile Ala Asp Asn Ala Leu Ser Gln Gly
          85           90           95

Ala Ala Ser Ser Glu Ser Ile Thr Ser Gln Ser Thr Ser Gln Glu Leu
100          105          110

Pro His Arg Arg Arg Lys Arg Leu Lys Glu Glu Ala Ala Lys Asn Asn
115          120          125

Ala Ala Glu Thr Glu Leu Pro Pro Asp Ala Ser Ser Gln Leu Ser Thr
130          135          140

Leu Ser Ser Ala Leu Pro Ala Thr Ser Leu Arg Arg Lys Leu Ala Ala

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145		150		155		160									
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Thr	Thr	Ser	Ala	Tyr	Gly	Met	Tyr	Pro	Ile	Ser	Ser	Leu	Leu	Thr	Leu
			180					185					190		
Asp	Pro	Ser	Met	Thr	Pro	Leu	Pro	Thr	Leu	Ser	Thr	Ser	Thr	Leu	Thr
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Phe	Leu	Tyr	Leu	Thr	Thr	Gly	Thr	Phe	Leu	Ser	Ser	Cys	Ser	Ala	Asn
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Val	Leu	Phe	Ala	Ile	Ala	Thr	Ala	Ala	Ala	Gly	Leu	Gly	Leu	Leu	Tyr
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Ile	Gly	Thr	Asn	Pro	Thr	Thr	Thr	Ala	Leu	Ser	Ala	Ser	Asn	Ile	Cys
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305					310					315					320
Thr	Ala	Ala	Ala	Gly	Gln	Thr	Ala	Thr	Thr	Gly	His	Asp	Ser	Trp	Arg
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Asp	Met	Leu	Phe	Ser	Lys	Asp	Ser	Ile	Gly	Gly	Trp	Leu	Leu	Gly	Gly
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Ile	Leu	Phe	Ala	Trp	Gln	Phe	Pro	His	Phe	Asn	Ala	Leu	Ser	Tyr	Met
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Phe	Pro	Phe	Ser	Val	Gly	Leu	Trp	Trp	Val	Gly	Val	Val	Gly	Asn	Gly
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Tyr	Lys	Phe	Trp	Arg	His	Gln	Gly	Ala	Asn	Gly	Ser	Ala	Arg	Arg	Leu
		435					440					445			
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	450					455					460				
Val	Thr	Lys	Lys	Gly	Leu	Trp	Asp	Gly	Val	Trp	Asn	Asn	Val	Phe	Gly
465					470					475					480

Gln Pro Val Glu Asp Glu Asp Asp Tyr Leu Trp Glu Asp Glu Asp Glu  
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Val Ala Glu Ala Glu Arg Lys Met Ile Pro Ala Lys Thr Ser Ser Ser  
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<210> 167

<211> 2679

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA266; clone 2-10-18; contig 4898 region 329309-331987  
Genomic sequence containing 3' and 5'-ends and the coding region

<400> 167

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atctctttat	ctgattcgat	caataccggg	agtactgcaa	ggaggacaag	tagacaggca	180
cttcgagaa	tccgtgagaa	agcaagggtac	agaagagaac	tactccgtac	tctgtactct	240
gtagagaaa	gcaggaggtt	caaacatgat	tggcccggtg	agaataagaa	aatatcatgc	300
cttaggtcca	aaggctagt	ctcacatgac	cttatcagtt	gagtcagggtg	atcttatcgt	360
tgtcccagag	agatgtgaag	aattattgca	ccggggagca	cgcaaggaaa	ccattctatc	420
ctatctcgtc	cctttagatt	accacaggac	atctacatct	tgaaccttac	cattccaaat	480
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atcccactga	tgcgcagca	atgcgcttgg	gctttgtctt	tgcgtctctc	tctcctgcac	600
ctctcttctc	aacagcacct	ttccgtcgac	agttgcatgc	ttccggcgctc	cgatcaattg	660
aacctgttat	ctttcgaaat	agccttgaaa	agactcttga	ggctcatcga	tcctccaatc	720
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aagaagagac	aagccaggcc	agggcaaaa	tagtctatga	catgaattca	acgatcaaga	2520
tcacgccggt	gtatgagaac	tccagggtta	gcaataccaa	caatcgacat	gtatggcacc	2580

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gcaaggaaaa gcaccgcgga accatacagag gatatacgat cgatcaattg ctgcccctct 2640
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<210> 168
<211> 1629
<212> DNA
<213> Aspergillus fumigatus

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<220>
<223> Phylum CEA266; clone 2-10-18; contig 4898 region 329309-331987
      Genomic sequence containing the coding region

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<400> 168
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<210> 169
<211> 1629
<212> DNA
<213> Aspergillus fumigatus

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<220>
<223> Phylum CEA266; clone 2-10-18; contig 4898 region 329309-331987
      Coding region without exons

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<400> 169
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gctggtcatt atcaatcacc tcaaaaggcc tcctccgtgt caaatgcaga gtcagagtcc 360
ccccggtctt ctgcgcctgc gagacgagcg cagaggaagg cccgttcgcc cagccaagta 420

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<210> 170

<211> 542

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA266; clone 2-10-18; contig 4898 region 329309-331987  
Protein sequence

<400> 170

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Asp Arg Ala Ala Met Arg Leu Gly Phe Ala Leu Arg Leu Ser Ser Pro  
20 25 30

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35 40 45

Gly Val Arg Ser Ile Glu Pro Val Ile Phe Arg Asn Ser Leu Glu Lys  
50 55 60

Thr Leu Glu Ala His Arg Ser Ser Asn Arg Ala Ser Leu Ile Arg Lys  
65 70 75 80

Val Ile Asn His Asp Cys Pro Ala Glu Thr Pro Pro Pro Ile Leu Pro  
85 90 95

Leu Glu Asn Arg Ala Gly His Asp Gln Ser Ser Gln Lys Ala Ser Ser  
100 105 110

Val Ser Asn Ala Glu Ser Glu Ser Pro Arg Ser Ser Ala Pro Ala Arg  
115 120 125

Arg Ala Gln Arg Lys Ala Arg Ser Pro Ser Gln Val Ala Thr Pro Gln  
130 135 140

Pro Gln Thr Thr Glu Tyr Pro Gln Leu Gln Trp His Ala Asp Glu Thr



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	180	185	190			
Leu Glu Leu Tyr Met Thr Pro Thr Pro Ser Glu Arg Thr Glu Ile Asp						
	195	200	205			
Arg Leu Val Ala Asp Met Gly Arg Leu Leu Ala Gly Ile Val Pro Ser						
	210	215	220			
Pro Pro Gln Val Thr Gly Ser Trp Arg Thr Arg Phe Ala Leu Ser His						
	225	230	235			240
Ser Gly Leu Asp Phe Val Leu Pro Val Pro Asp Ser Asp Arg Ser Thr						
	245	250	255			
Arg Asp Val Arg Lys Pro Ser Ala Thr Arg Pro Lys Val Leu Gln Thr						
	260	265	270			
Tyr Lys Lys Leu Leu His Glu Val Gly His Ala Leu Gln Gln Ser Pro						
	275	280	285			
Ser Phe Ala Glu Arg Val Arg Ile Ile Gly Ser Arg Phe Pro Val Leu						
	290	295	300			
Ser Ala Ile His Arg Pro Thr Gly Arg Leu Leu Gln Phe His Cys Gly						
	305	310	315			320
Glu Gly Leu Pro Ala Ser Val Glu Tyr Ile Met Asp Tyr Gln Ala Glu						
	325	330	335			
Tyr Pro Ser Ile Arg Pro Leu Tyr Val Thr Ala Arg Leu Ile Leu Glu						
	340	345	350			
Ala Arg Gly Arg Tyr Gly Arg Thr Gln Met Ser Ile Glu Ser Asp Ala						
	355	360	365			
Leu Val Met Leu Leu Val Ala Phe Leu Lys Met Asn His Gly Arg Phe						
	370	375	380			
Gln Arg Pro Asp Cys Leu Gly Glu Gln Leu Ile Ala Phe Leu Arg Ala						
	385	390	395			400
Tyr Gly Ser Asp Ile Asp Leu Thr Thr Thr Gly Val Ser Val Asp Pro						
	405	410	415			
Pro Ser Trp Phe Asn Ala Ser Thr Val Lys Arg Ala Ser Ala Leu Tyr						
	420	425	430			
Ala Pro Asp Asp Leu Pro Ala His Leu Arg Gly Gln Arg Ser Leu Ile						
	435	440	445			
Ser Leu Lys Arg Thr Ala Ala Ala Arg Arg Asn Leu Pro Ala Ala Ser						
	450	455	460			
Arg Leu Cys Val Gln Asp Pro Thr Asn Tyr Met Asn Asp Leu Gly Arg						
	465	470	475			480

Ser Cys Val Arg Thr Leu Glu Leu Gln His Thr Phe Ser Leu Ala His  
                             485                            490                            495

Asp Arg Leu Gly Ala Ser Leu Lys Arg Trp Asp Asp Ser Glu Pro Ala  
                             500                            505                            510

Ala Asn Val Ser Ile Leu Thr Arg Ala Leu Gln Ala Asn Phe Ser Asp  
                             515                            520                            525

Phe Glu Asn Leu Arg Ala Lys Ser Leu Lys Leu Asn Ala Thr  
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<210> 171  
 <211> 1573  
 <212> DNA  
 <213> *Aspergillus fumigatus*

<220>  
 <223> Phylum CEA280; clone 6-8-13; contig 4925 region 997952-996381  
 Genomic sequence containing 3' and 5'-ends and the coding region

<220>  
 <223> misc\_feature  
 <223> (683)..(683)  
 <223> n is a, c, g, or t

<400> 171

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cgcgcccccg	accgaccatt	ttggacttgg	ttagtaagct	ccagtgacca	gaaagcttac	120
cagctagctt	cacttgagat	atcacaagat	gctttgggtc	gcctgccacg	aggtcttgct	180
ccatgtcaac	cacgaggatt	cagtctctgc	ctcatctcag	tccaggcgag	gtttctttgc	240
tggatcttgc	ggctgatgac	cctcgcgatg	tggtgtccct	gtccgacaag	gaagcgttga	300
ttttgcagct	ctacaatcaa	atccaggaac	tggaactgga	aaaggcactt	cttgaacaag	360
gtacgcgtca	aatttatatt	ttttgtaatt	ttcttttttt	tgtttctctg	atgtagcttc	420
ttggggccctc	caaatctgtc	agcccagggt	actgattccc	actagagctg	gaaccggctt	480
ctgggggacaa	tctggatgag	caacttgcaa	tgcgagaacg	tgagcttctc	gaggcaaggg	540
ccacgtacac	ggtcaggaga	aaggccacca	gtactgtcct	gatgactgat	ccaacattaa	600
aagctgttca	cttgaaagct	atatcacctg	ttgaaagggt	ttacctcctt	tcagtttatg	660
cgagcatttc	aattctgcat	tcnctatac	taacgcttca	tagagctctt	ctacccttgg	720
tcaaccggcg	tgatgtgttg	tctttggcac	atgagaacct	aatgaatgcg	cacaacgcga	780
ctttgagggg	actatccaat	ttagaagtac	aaaatctaga	gctacaccag	aggaatcaag	840
agctagcgcg	gcagcttctt	gagtcgcgca	aggatgatga	ttcatggaga	gaagcactgg	900
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caagatggga	agtcatgaaa	agcgttgcaa	gtgctattgt	tgtgggaagt	ggagtgaact	1020
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cctcgaaatt	aatgatttcg	aacaatttgg	tagtattgac	ttctccgacc	ggcgctactac	1140
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cggatatatac	acagtatcgt	cttggtcgaa	tcagcagaac	ggctgaggaa	gctcggtttag	1260
gtaccgtaag	tgtcgcccg	actgcccata	acctgaagac	gcgccagcgc	ccactagaac	1320
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gccctgaagc	cctggaatca	tggagaaaat	togaatacag	atggaaggca	attagaaccc	1500
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<210> 172  
 <211> 573  
 <212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA280; clone 6-8-13; contig 4925 region 997952-996381  
Genomic sequence containing the coding region

<220>

<223> misc\_feature

<223> (183)..(183)

<223> n is a, c, g, or t

<400> 172

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atatcacctg	ttgaaagggt	ttacctcctt	tcagtttatg	cgagcatttc	aattctgcat	180
tcncctatac	taacgcttca	tagagctctt	ctacccttgg	tcaaccggcg	tgatgtgttg	240
tctttggcac	atgagaacct	aatgaatgcg	cacaacgcga	ctttgaggga	actatccaat	300
ttagaagtac	aaaatctaga	gctacaccag	aggaatcaag	agctagcgcg	gcagcttctt	360
gagtccgcga	aggatgatga	ttcatggaga	gaagcactgg	atgatgacga	cctcaaggca	420
caacttgagc	agctagaggc	cgatcgcaaa	aagagcaaat	caagatggga	agtcatgaaa	480
agcgttgcaa	gtgctattgt	tgtgggaagt	ggagtgaact	gggctgaaga	cgatgagctt	540
acagctctag	tcattgatga	atctgatgat	taa			573

<210> 173

<211> 573

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA280; clone 6-8-13; contig 4925 region 997952-996381  
Coding region without exons

<220>

<223> misc\_feature

<223> (183)..(183)

<223> n is a, c, g, or t

<400> 173

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atatcacctg	ttgaaagggt	ttacctcctt	tcagtttatg	cgagcatttc	aattctgcat	180
tcncctatac	taacgcttca	tagagctctt	ctacccttgg	tcaaccggcg	tgatgtgttg	240
tctttggcac	atgagaacct	aatgaatgcg	cacaacgcga	ctttgaggga	actatccaat	300
ttagaagtac	aaaatctaga	gctacaccag	aggaatcaag	agctagcgcg	gcagcttctt	360
gagtccgcga	aggatgatga	ttcatggaga	gaagcactgg	atgatgacga	cctcaaggca	420
caacttgagc	agctagaggc	cgatcgcaaa	aagagcaaat	caagatggga	agtcatgaaa	480
agcgttgcaa	gtgctattgt	tgtgggaagt	ggagtgaact	gggctgaaga	cgatgagctt	540
acagctctag	tcattgatga	atctgatgat	taa			573

<210> 174

<211> 190

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA280; clone 6-8-13; contig 4925 region 997952-996381  
Protein sequence

<400> 174

Gln Leu Ala Ile Ala Glu Arg Glu Leu Leu Glu Ala Arg Ala Thr Tyr  
 1 5 10 15  
 Thr Val Arg Arg Lys Ala Thr Ser Thr Val Leu Met Thr Asp Pro Thr  
 20 25 30  
 Leu Lys Ala Val His Leu Lys Ala Ile Ser Pro Val Glu Arg Phe Tyr  
 35 40 45  
 Leu Leu Ser Val Tyr Ala Ser Ile Ser Ile Leu His Ser Pro Ile Leu  
 50 55 60  
 Thr Leu His Arg Ala Leu Leu Pro Leu Val Asn Arg Arg Asp Val Leu  
 65 70 75 80  
 Ser Leu Ala His Glu Asn Leu Met Asn Ala His Asn Ala Thr Leu Arg  
 85 90 95  
 Glu Leu Ser Asn Leu Glu Val Gln Asn Leu Glu Leu His Gln Arg Asn  
 100 105 110  
 Gln Glu Leu Ala Arg Gln Leu Leu Glu Ser Ala Lys Asp Asp Asp Ser  
 115 120 125  
 Trp Arg Glu Ala Leu Asp Asp Asp Asp Leu Lys Ala Gln Leu Glu Gln  
 130 135 140  
 Leu Glu Ala Asp Arg Lys Lys Ser Lys Ser Arg Trp Glu Val Met Lys  
 145 150 155 160  
 Ser Val Ala Ser Ala Ile Val Val Gly Ser Gly Val Asn Trp Ala Glu  
 165 170 175  
 Asp Asp Glu Leu Thr Ala Leu Val Ile Asp Glu Ser Asp Asp  
 180 185 190

<210> 175

<211> 2593

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.1; clone 5-3-11; contig 4839 region 10030-12622  
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 175

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gcttcgactg	gaaattcgga	gatcgccata	tatttgagtt	atgtaagcac	cgccgcaggc	180
gtctcattgg	gctggggaag	ctatcaacaa	ccaccagag	cttcttgaac	ttaaactcgg	240
gggtgcatga	ctaatagttt	caataatgga	cgtcggatgc	tttgtaaatac	aacggcggtc	300
ctacaatggg	gatctatgca	cagttcggtta	cataggtaaa	gttgagggca	ccaccggcga	360
gtggctcgga	gtggaatggg	atgacccac	gcgggggaag	cattctggag	aacacaacgg	420
agtgagatat	ttacatgta	tgaaagtatt	ttcaagactg	gatagagcgg	attgactgac	480
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gaccgacaga	cctcgaggct	tccttgaggc	agtgcgtcac	aagtatgctt	ctgagttcca	600
agaagaactc	gcaagacagc	agtcaggcga	agtctctgct	gcgcgggaaa	tcatcaaatt	660
tagtagcaaaa	gtagtggaag	aggtcggctt	cgacaagatc	cggaagaaac	ttgcagagct	720
ccaggaattg	aaaatcgatc	tcctggatcg	cctatgcatc	gcaggagtgc	tcctcatag	780
agcgagtcta	catgagcttg	cagaggcttg	caaggagata	gaacagacat	gtcctaagat	840

cgttgacctc	gatctgagtt	acaacttact	ggaaagctgg	gttgacattg	caaacatatg	900
tcaacagctg	aagcgcttga	agacattgaa	gctgatgttg	gtcattcagt	acatctgtga	960
gaagcatgct	gacagttggc	agcggaaatc	gtctaggtcc	tcgacaggag	ggtctgatat	1020
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gcacaaagct	actgcttggg	taccagtga	ctgactgact	cttgggtccc	tttagatttc	1140
agctttgaca	tatcaattcc	cgctactctc	tgctctgtct	gcctccgcaa	atcagattac	1200
ccagatcttg	acacctatca	cggataccat	cacgaccttg	acactggaaa	acaatgacat	1260
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ttccgaaaaat	ctcagatcgg	tggacctatc	cagaaacaat	atcgattctt	ggctgtttgt	1440
gaatgaactt	caacgcgtat	ttcctgggct	gcaatctttg	cgcataatcag	gaaatcccct	1500
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aagctggagg	gcaacactga	ctgctgtttt	aggactaggt	cggttttggg	tggcagatta	2520
tcaccgcaac	tgttttgtga	taacagtgat	atcatttccc	tttcatataa	caatttaata	2580
ctcagacatc	gtc					2593

&lt;210&gt; 176

&lt;211&gt; 1974

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA281.1; clone 5-3-11; contig 4839 region 10030-12622  
Genomic sequence containing the coding region

&lt;400&gt; 176

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cccacgcggg	ggaagcattc	tggagaacac	aacggagtga	gatattttac	atgtatgaaa	180
gtattttcaa	gactggatag	agcggattga	ctgacttgaa	cggaaaggtag	aaggaaacac	240
cccacggctg	gttcgttcgt	gcgccttctg	cgacggaccg	acagacctcg	aggcttcctt	300
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ggcgaagtct	ctgctgcgcg	ggaaatcatc	aaatttagta	gcaaagtagt	ggaagaggtc	420
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gatcgcctat	gcacgcaggg	agttctccct	catagagcga	gtctacatga	gcttgacagag	540
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caacccgata	ctgttgaggc	aaggatcaga	gtagaagttg	caacatcgaa	ttga	1974

&lt;210&gt; 177

&lt;211&gt; 1830

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA281.1; clone 5-3-11; contig 4839 region 10030-12622  
Coding region without exons

&lt;400&gt; 177

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aaacacccca	cggctgggtc	gttcgtgcgc	ccttcgcgac	ggaccgacag	acctcgaggc	240
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cacctctcgc	tgagagagaa	tcgtatcggg	aaagtctatg	cgtctggcat	ggaaggaaac	960
tctcttcagt	tttccgaaaa	tctcagatcg	gtggacctat	ccagaaacaa	tatcgattct	1020
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catccccgct	atcaggagct	ttgtgagaaa	tacggagcgc	ccacaatcag	gagagccgag	1380
ctggcaggcg	ctgccgtgaa	tccgcgctct	gttgccgccc	gagtagtgaa	gttggctttt	1440
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ccgagatcct	ttaatacata	tcaagtcaag	gcaatcgcct	cccgcctgtt	caatttgccg	1560
ccttaccagt	gccgactagt	ctgggagacc	aacgagttag	accctattca	tcaggagaaa	1620
aaggacgatg	gagacgattg	ggatagtgat	gaggatgaag	ccacagctat	tggattgggg	1680
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ctcctggatt	caacgcgaga	cataggcttt	tggttccaac	ccgatactgt	tgaggcaagg	1800
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&lt;210&gt; 178

&lt;211&gt; 609

&lt;212&gt; PRT

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA281.1; clone 5-3-11; contig 4839 region 10030-12622  
Protein sequence

&lt;400&gt; 178

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Trp Leu Gly Val Glu Trp Asp Asp Pro Thr Arg Gly Lys His Ser Gly
          35          40          45

Glu His Asn Gly Val Arg Tyr Phe Thr Cys Arg Arg Lys His Pro Thr
          50          55          60

Ala Gly Ser Phe Val Arg Pro Ser Arg Arg Thr Asp Arg Pro Arg Gly
65          70          75          80

Phe Leu Glu Ala Val Arg His Lys Tyr Ala Ser Glu Phe Gln Glu Glu
          85          90          95

Leu Ala Arg Gln Gln Ser Gly Glu Val Ser Ala Ala Arg Glu Ile Ile
          100          105          110

Lys Phe Ser Ser Lys Val Val Glu Glu Val Gly Phe Asp Lys Ile Arg
          115          120          125

Lys Lys Leu Ala Glu Leu Gln Glu Leu Lys Ile Val Leu Leu Asp Arg
          130          135          140

Leu Cys Ile Ala Gly Val Leu Pro His Arg Ala Ser Leu His Glu Leu
          145          150          155          160

Ala Glu Ala Cys Lys Glu Ile Glu Gln Thr Cys Pro Lys Ile Val Asp
          165          170          175

Leu Asp Leu Ser Tyr Asn Leu Leu Glu Ser Trp Val Asp Ile Ala Asn
          180          185          190

Ile Cys Gln Gln Leu Lys Arg Leu Lys Thr Leu Lys Leu Met Leu Val
          195          200          205

Ile Gln Tyr Ile Cys Glu Lys His Ala Asp Ser Trp Gln Arg Lys Ser
          210          215          220

Ser Arg Ser Ser Thr Gly Gly Ser Asp Ile Arg Arg Tyr His Asn Thr
          225          230          235          240

Thr Leu Gly Arg Asp Ser Thr Arg Met Gly Arg Gly Met Leu His Lys
          245          250          255

Ala Thr Ala Trp Leu Pro Ile Thr Gln Ile Leu Thr Pro Ile Thr Asp
          260          265          270

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Thr Ile Thr Thr Leu Thr Leu Glu Asn Asn Asp Ile Ser Ser Leu Ser  
 275 280 285  
 Ser Leu Ala Cys Leu Thr Ser Leu Ser Lys Leu Glu His Leu Ser Leu  
 290 295 300  
 Arg Glu Asn Arg Ile Gly Lys Val Tyr Ala Ser Gly Met Glu Gly Asn  
 305 310 315 320  
 Ser Leu Gln Phe Ser Glu Asn Leu Arg Ser Val Asp Leu Ser Arg Asn  
 325 330 335  
 Asn Ile Asp Ser Trp Leu Phe Val Asn Glu Leu Gln Arg Val Phe Pro  
 340 345 350  
 Gly Leu Gln Ser Leu Arg Ile Ser Gly Asn Pro Leu Tyr Asp Lys Pro  
 355 360 365  
 Val Ala Pro Ser Asn Val Thr Asn Leu Pro Glu Lys Pro Met Thr Val  
 370 375 380  
 Asp Glu Ala Tyr Met Leu Thr Leu Ser Arg Leu Ala Ser Ile Gln Thr  
 385 390 395 400  
 Leu Asn Tyr Ser Lys Ile Thr Ser Gln Asp Arg Ser Asn Gly Glu Leu  
 405 410 415  
 Tyr Tyr Leu Ser Leu Ile Gly Lys Glu Leu Ser Ala Tyr Pro Glu Ser  
 420 425 430  
 Ala Glu Arg Glu Ile Leu Ala Thr His Pro Arg Tyr Gln Glu Leu Cys  
 435 440 445  
 Glu Lys Tyr Gly Ala Pro Thr Ile Arg Arg Ala Glu Leu Ala Gly Ala  
 450 455 460  
 Ala Val Asn Pro Arg Ser Val Ala Ala Arg Val Val Lys Leu Ala Phe  
 465 470 475 480  
 Cys Leu His Ser Ser Val Ser Ser Gly Ala Asn Gln Glu Gln Phe Arg  
 485 490 495  
 Val Gln Lys Ile Pro Arg Ser Phe Asn Thr Tyr Gln Val Lys Ala Ile  
 500 505 510  
 Ala Ser Arg Leu Phe Asn Leu Pro Pro Tyr Gln Cys Arg Leu Val Trp  
 515 520 525  
 Glu Thr Asn Glu Leu Asp Pro Ile His Gln Glu Lys Lys Asp Asp Gly  
 530 535 540  
 Asp Asp Trp Asp Ser Asp Glu Asp Glu Ala Thr Ala Ile Gly Leu Gly  
 545 550 555 560  
 Glu Ser Asn Lys Leu Thr Pro Ala Thr Glu Asp Gly Lys Phe Ile Arg  
 565 570 575  
 Arg Glu Val Glu Leu Leu Asp Ser Thr Arg Asp Ile Gly Phe Trp Phe  
 580 585 590  
 Gln Pro Asp Thr Val Glu Ala Arg Ile Arg Val Glu Val Ala Thr Ser



595

600

605

Asn

&lt;210&gt; 179

&lt;211&gt; 1867

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA281.2; clone 5-3-11; contig 4839 region 12269-14135  
Genomic sequence containing 3' and 5'-ends and the coding region

&lt;400&gt; 179

caactat	tttc	gacataggag	ttgtgaagga	gttccttaac	ctacattgtc	gcgggtggg	60
taatatata	at	agttgagcac	gactcgtgcg	ttaggataca	acgaggtcaa	cgacagaaaa	120
gtagaacctc	ttacgcaagc	gcctgtggcc	tctgttaacc	gaatggattt	agaggccttc		180
ttggttattc	ttaaacaata	tgatatgtgt	agtgtatatt	caagctggag	ggcaaacactg		240
actgctgttt	taggactagg	tcggtttttg	gtggcagatt	atcaccgcaa	ctgttttgtg		300
ataacagtga	tatcatttcc	ctttcatata	acaatttaac	actcagacat	cgatcatggca		360
gaataactgga	aatcagctgt	aagtgcctt	cattcagttc	cgcagacttc	ttcgtgataa		420
tctttacgtg	gggaagtccg	gcatcaactg	acagcaatat	tctagccccg	gttctgggtgc		480
aaacaatgca	agatattcat	tcgggataca	cccttcgaga	aaaccagca	tgaagcgagt		540
gccaaacacc	agggaaacct	taagcgtttc	ctacgagata	tccaccggga	aaatgaacgg		600
aagcaaagag	aaactcagaa	ggcgaaggat	gaagtcgagc	gattaaggca	aactgtcgca		660
ggaaaaccag	gtgcaaaaga	cagcggcgca	acagcttgga	aacacgcctc	ggctgcccct		720
ccaccggcag	aacgacctgt	gtccctggaa	gagagaaaga	agcagatagc	gcagctggca		780
gagatgggaa	ttgctatccc	ggacgaatac	cgtggtgaac	tcgcgctcgc	tggcgaatgg		840
cagacggtat	ccgaacgagt	tattcgacca	gatgacgata	cagaggaagg	aaagcctggt		900
agctctatcg	gcgttcggaa	acgcaagatg	gaaggcgatg	aggaggagca	ggaggcgcgca		960
caggagggccg	agagattcgt	gagtcagggt	tggggctcga	ggactcggca	gtatcctggg		1020
gagcagagcg	atgcagacct	ggatgcactt	ctaaattcta	ccaaggatgt	aaagaaggtc		1080
aagttgtcgg	cgccggatga	agggtcgaaa	gagaaggcta	gcaaagaggg	tgctacacca		1140
agcaacgata	cggaccaggc	tgcggtcag	gagtcagAAC	taccatcagt	caagtctgag		1200
ggtaaagaag	cggcgagct	tgctacaaca	gataccccag	cgggtgaagca	ggaagaggag		1260
gcggcaccta	caggagttgt	ttttaagaag	cgcaagccga	aggtcctgag	gaaatagtcg		1320
aatttgcagc	tgctggatat	ctattatcta	ccatgcgcac	aaatgtacag	atgatgcgtt		1380
atggttgcgc	acggtccaat	atgcctcgcc	tgccggtgct	cacatgaagc	gatcatgggt		1440
tcttgtctca	ctgcgctcca	gtgttcgaaa	accgggatga	tgctctggc	ctccagtcgt		1500
ccgtcgccga	agcaaccag	ctcatagaag	atctggattc	tcgattcgct	tgcgcgaaa		1560
gcctagtctg	gtcttgcgtt	agcctatata	cagattgagt	gtatcgattc	gagcttatgc		1620
gggttgtctg	ataatattct	gccttacatt	ggcagagaga	cgttgagca	cataggggtg		1680
atggagaatg	atcagttctt	acgtatgtaa	gcatgatgtc	tagctcagaa	aagagtccca		1740
tataccatgc	gactcgttgg	cagcatccac	ctcttccttt	ggagtgcaat	ctacaatagc		1800
atgcatacga	aacaaatttc	gttgacaagg	agaccagagg	cgagaagagt	aatatagcaa		1860
gccagct							1867

&lt;210&gt; 180

&lt;211&gt; 963

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA281.2; clone 5-3-11; contig 4839 region 12269-14135  
Genomic sequence containing the coding region

&lt;400&gt; 180

atggcagaat	actggaaatc	agctgtaagt	gcccttcatt	cagttccgca	gactttcttcg	60
tgataatctt	tacgtgggga	agtccggcat	caactgacag	caatattcta	gccccgggtc	120

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tgggtgcaaac aatgcaagat attcattcgg gatacacctt tcgagaaaac ccagcatgaa 180
gcgagtgcc aacaccaggg aaaccttaag cgtttcctac gagatatcca ccgggaaaat 240
gaacggaagc aaagagaaac tcagaaggcg aaggatgaag tcgagcgatt aaggcaaaact 300
gtcgcaggaa aaccagggtg aaaagacagc ggcgcaacag cttggaaaca cgcctcggct 360
gcccctccac cggcagaacg acctgtgtcc ctggaagaga gaaagaagca gatagcgag 420
ctggcagaga tgggaattgc tatcccgagc gaataccgtg gtgaactcgc gctcgctggc 480
gaatggcaga cggatatccga acgagttatt cgaccagatg acgatacaga ggaaggaaag 540
cctggtagct ctatcggcgt tcggaaaacgc aagatggaag gcgatgagga ggagcaggag 600
gcgcgacagg aggccgagag attcgtgagt cagggttggg gctcgaggac tcggcagtat 660
cctggggagc agagcgatgc agacctggat gcacttctaa attctaccaa ggatgtaaag 720
aaggtcaagt tgtcggcgcc ggatgaaggg tcgaaagaga aggctagcaa agaggggtgt 780
acaccaagca acgatacggg ccaggctgcg gctcaggagt cagaactacc atcagtcaag 840
tctgagggta aagaagcggc gcagcttgct acaacagata cccagcggg gaagcaggaa 900
gaggagcgcg cacctacagg agttgttttt aagaagcgca agccgaaggc cctgaggaaa 960
tag 963

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<210> 181

<211> 876

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.2; clone 5-3-11; contig 4839 region 12269-14135  
Coding region without exons

<400> 181

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atggcagaat actggaaaac agtcccccg ttctggtgca aacaatgcaa gatattcatt 60
cgggatacac ctttcgagaa aaccagcat gaagcgagt ccaaacacca gggaaacctt 120
aagcgtttcc tacgagatat ccaccgggaa aatgaacgga agcaaagaga aactcagaag 180
gcgaaggatg aagtcgagcg attaaggcaa actgtcgag gaaaaccagg tgcaaaagac 240
agcggcgcaa cagcttgga acacgcctcg gctgcccctc caccggcaga acgacctgtg 300
tccctggaag agagaaagaa gcagatagcg cagctggcag agatgggaat tgctatcccg 360
gacgaatacc gtggtgaact cgcgctcgct ggogaatggc agacggtatc cgaacgagtt 420
attcgaccag atgacgatac agaggaagga aagcctggta gctctatcgg cgttcgaaa 480
cgcaagatgg aaggcgatga ggaggagcag gaggcgcgac aggaggccga gagattcgtg 540
agtcagggtt ggggctcgag gactcggcag tatectgggg agcagagcga tgcagacctg 600
gatgcacttc taaattctac caaggatgta aagaaggta agttgtcggc gccggatgaa 660
gggtcgaaaag agaaggctag caaagagggt gctacaccaa gcaacgatac ggaccaggct 720
gcggctcagg agtcagaact accatcagtc aagtcagag gttaaagaagc ggcgcagctt 780
gtacaacag atacccagc ggtgaagcag gaagaggagg cggcacctac aggagttgtt 840
tttaagaagc gcaagccgaa ggtcctgagg aaatag 876

```

<210> 182

<211> 291

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA281.2; clone 5-3-11; contig 4839 region 12269-14135  
Protein sequence

<400> 182

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Met Ala Glu Tyr Trp Lys Ser Ala Pro Arg Phe Trp Cys Lys Gln Cys
1           5           10           15

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Lys Ile Phe Ile Arg Asp Thr Pro Phe Glu Lys Thr Gln His Glu Ala
20           25           30

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Ser Ala Lys His Gln Gly Asn Leu Lys Arg Phe Leu Arg Asp Ile His  
           35                                  40                                  45  
 Arg Glu Asn Glu Arg Lys Gln Arg Glu Thr Gln Lys Ala Lys Asp Glu  
   50                                  55                                  60  
 Val Glu Arg Leu Arg Gln Thr Val Ala Gly Lys Pro Gly Ala Lys Asp  
   65                                  70                                  75                                  80  
 Ser Gly Ala Thr Ala Trp Lys His Ala Ser Ala Ala Pro Pro Pro Ala  
                                   85                                  90                                  95  
 Glu Arg Pro Val Ser Leu Glu Glu Arg Lys Lys Gln Ile Ala Gln Leu  
                                   100                                  105                                  110  
 Ala Glu Met Gly Ile Ala Ile Pro Asp Glu Tyr Arg Gly Glu Leu Ala  
                                   115                                  120                                  125  
 Leu Ala Gly Glu Trp Gln Thr Val Ser Glu Arg Val Ile Arg Pro Asp  
   130                                  135                                  140  
 Asp Asp Thr Glu Glu Gly Lys Pro Gly Ser Ser Ile Gly Val Arg Lys  
   145                                  150                                  155                                  160  
 Arg Lys Met Glu Gly Asp Glu Glu Glu Gln Glu Ala Arg Gln Glu Ala  
                                   165                                  170                                  175  
 Glu Arg Phe Val Ser Gln Gly Trp Gly Ser Arg Thr Arg Gln Tyr Pro  
                                   180                                  185                                  190  
 Gly Glu Gln Ser Asp Ala Asp Leu Asp Ala Leu Leu Asn Ser Thr Lys  
   195                                  200                                  205  
 Asp Val Lys Lys Val Lys Leu Ser Ala Pro Asp Glu Gly Ser Lys Glu  
   210                                  215                                  220  
 Lys Ala Ser Lys Glu Gly Ala Thr Pro Ser Asn Asp Thr Asp Gln Ala  
   225                                  230                                  235                                  240  
 Ala Ala Gln Glu Ser Glu Leu Pro Ser Val Lys Ser Glu Gly Lys Glu  
                                   245                                  250                                  255  
 Ala Ala Gln Leu Ala Thr Thr Asp Thr Pro Ala Val Lys Gln Glu Glu  
                                   260                                  265                                  270  
 Glu Ala Ala Pro Thr Gly Val Val Phe Lys Lys Arg Lys Pro Lys Val  
                                   275                                  280                                  285  
 Leu Arg Lys  
   290

<210> 183

<211> 2193

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.1; clone 10-4-20; contig 4929 region 328110-325663  
 Genomic sequence containing 3' and 5'-ends and the coding region

&lt;400&gt; 183

gagcaactgc	cagaaatcca	gacgtgcaac	tctctcgcaa	aaaaaagcgt	tgtctcccaa	60
aacggagggt	gttaagttat	cgccacgggg	aaatagccca	aaaggaactc	gtcacagctg	120
gaatcaacac	caagtaccga	agaaacaagc	gagcagcggc	tgtttggtt	ctgcagctgc	180
acaaaaaatg	ggaacgaagt	gaatgaggtt	agatagagat	gaggatggat	caagaagcgc	240
cctccagatg	tagcaatgaa	gagatgatgt	tgcaagaaga	ggtgaaacaa	gctggcggca	300
cgggatcagg	ctaggctaga	tagggtttagc	aacgaggggtg	acatcacgtg	agaacgggca	360
tcgtgatatg	gatgacaatt	aacatcataa	acactcttcg	ttcagttgct	gtgactcctg	420
acgcgtaagg	ggatctgggg	tgaagtcaag	caatagactc	tctgacagat	ttgacttttag	480
agaaagtaaa	taacaccact	atggacatct	cgcaagaaac	cgttgataaa	atacgacgtt	540
tcgcgcaaaa	gcgccaaaaa	gcgaggaggt	tctacgagga	acactcggta	aatccagcta	600
atthttgacgc	ttacaatcgc	aagttggatg	agacgttggc	agagctgcag	gctcaagtca	660
aacgtcatga	ggatgagctc	cgcaagggtac	gtcaacaagt	tgccctagaat	ataagccgac	720
tgtcacaaga	gatttcatgc	atgaattagg	aatactgaca	agaggaacag	ctacgcatga	780
ccaccacgat	cgagttcgct	caaattgggg	cagatccttg	ggcccgcatc	tcagaagtgc	840
gcagagccaa	gaaagcgtat	gattctcttc	tgcaatcggg	aacgcgactg	ccgagtccag	900
gctcgccctt	gccttcatta	cttgcggttg	acgagggcgtc	tcgtctcgtc	aaggagagca	960
agacctcaat	ctcactgacg	gcgagagaaac	tgctctcgga	tcgtcagcgc	ttgaaagcgg	1020
aagaagccaa	tttgcgcgat	gcgcaactga	tcaaagacgg	ggttgagaaa	aggattgagc	1080
ggctgaacgc	agaaaaatcg	agtcaagtcc	agaaaaactcc	tgcgagctt	gcgtatgac	1140
tcgtcaagga	gcagcaggaa	aagatcgaga	gacttgatac	taccacagaa	gagctaaagt	1200
cctctctcta	taaatttgct	gaagacacac	ttgccccaat	gcttgctgca	gaaaatctgg	1260
gcggtcccac	tgtcggagat	gcgttggaag	tttcggacac	taccttaaaa	gcgggctaca	1320
ctagccatgg	gaagcctaag	aaacccaaaa	ctccggccgt	ggggacttct	gacagtggcc	1380
aacagcggat	tgacgagctt	gttcgtcgcc	aaactgcgca	ggagggcaac	gagcaggcaa	1440
cccttttgaa	caaaagagag	gcggccgcgc	ctgaaatgcg	agctcttctt	actgctctgt	1500
tagatgcgga	ttactcctat	gtcgaccttc	cgcacgagtc	agcggcctcg	cgctttctag	1560
taagagcgaa	ggtagctcaa	ttccatccgc	gcgatgccag	gaagcttcgg	ttaatgtatt	1620
ttgggcgctc	attagtcat	tgaggtggct	acatgtaccg	tactacatct	cccagcttac	1680
aaatggatatc	acatttcacc	aaacatctgg	gaaaagacaa	acagacgcca	tccccacgga	1740
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caacgaagaa	gcggccccga	aagccactgg	tagcataacg	ccttgagaat	gcgagagata	1860
catcaaaaagc	ttatcagaaa	gttcaatgct	cgaggtcaaa	aatataccgt	taatgccata	1920
caagaaacat	ggaagaagaa	agaccgtagc	cggttatcag	atcggcatca	ttccgatgct	1980
ggtagaagta	ctcttgcccg	tattctttgc	tttgagacca	gttcgggaac	ccgccgagcg	2040
cttggtgact	tgatcgctgg	gctcccttct	aggtcgcggc	gtttttattt	ttgaactcga	2100
ccctgtagcg	ttcttgcggt	ggaagcgctt	cttggaacgaa	gtctttcttt	tcttggaacg	2160
gctagtctcg	gtgtcttcat	actcttcgga	tga			2193

&lt;210&gt; 184

&lt;211&gt; 1448

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA282.1; clone 10-4-20; contig 4929 region 328110-325663  
Genomic sequence containing the coding region

&lt;400&gt; 184

atgtctgctt	ctccatccgc	actgcaatcg	accaagcggc	ccttgaggga	cccttcttcg	60
ccgtccggac	caaatgatca	gccagaagct	aaacgtcctg	ccttgacaaa	agtagtaaag	120
ggaaacgagt	cggagaccta	tacggatgcc	aaggctgagc	cttccgctgc	gccaagtgt	180
actgctgatg	gccagggcga	cactgttggt	cctgatgctc	caaatggtaa	gggtgcatcc	240
acggagacgc	agccaattca	gtcgaccgcg	tctcatggcg	agcgcgctac	ttctcagccc	300
gaacagcagc	gcccacaaga	tgaatccagc	tggaattcaca	ttcgcgctgt	aatttctagc	360
caggaagctg	ccacagtcac	tggcaagggt	ggagaaaaacg	tatctcagat	tcgtcgtttg	420
tctggagcaa	agtgcactgt	cagcgactac	tcccgtggtg	cagtcgaacg	tattttgacc	480
gtgagcggcc	cacaggatgc	cgttgccaag	gttggttttt	tgatctatcc	ttcgtgtgtt	540
gaaagattgc	taattcagag	taggcgtttg	gtttgatcat	ccgtacattg	aacaatgaac	600
ctcttgatgc	cccctctacc	gcccattcca	agacataccc	tctgcgtttg	ctgatcccc	660

atctccttat	tggtccatc	attggcaaag	gtggttcacg	cattcgcgaa	attcaggaag	720
cttctggtgc	cgcactgaat	gcatccgatt	cgtgccttcc	cttgtcctct	gagcggtcac	780
ttgtaattct	cggcgttgcc	gattctgtcc	acatcgctac	ctactacgtc	gccgtaacct	840
tcgttgagca	gctcactgag	cgctttggag	gtcctgcagc	ctcagcttat	gccactcgca	900
gcggtggccc	tgctggagca	gtgcctggcg	gtatgcaggt	tgtcccgtat	gttccacagc	960
ccgctgggtg	tcaatatggc	catccagaac	atctcaagag	acaccatcac	caccccaatc	1020
gcgctgctgc	aggcgcctat	ggggtccctt	accttcacgg	tcagcctgct	cccgcaccag	1080
tggtccagcc	ggctttgcat	tatggagctg	ctccccatgc	cccttacgca	ggagctggcc	1140
cccatcagcc	tgctccatac	ggcgcaccgc	agcccgcctca	ggcacgcggc	gctcctaccc	1200
ctgccacacc	cgttggaggt	gtcatgcctg	gtcagccatt	gactcagcag	atctacatcc	1260
ccaacgacat	ggttggtgcc	atcatcgga	agggcgggtg	gaagatcaat	gagattcgac	1320
acctcagtgg	cagtgtgatc	aagattaatg	agcctcaaga	gaacagcaat	gagcgtttgg	1380
tgactattac	tggaaaccag	gaatgcaacc	aaatggctct	gtacatgctt	tactcgcgac	1440
ttgggttag						1448

&lt;210&gt; 185

&lt;211&gt; 1395

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

&lt;223&gt; Phylum CEA282.1; clone 10-4-20; contig 4929 region 328110-325663

Coding region without exons

&lt;400&gt; 185

atgtctgctt	ctccatccgc	actgcaatcg	accaagcggc	ccttggagga	cccttcttcg	60
ccgtccggac	caaagtatca	gccagaagct	aaacgtcctg	ccttggacaa	agtagtaaaag	120
ggaaacgagt	cggagaccta	tacggatgcc	aaggctgagc	cttccgctgc	gccaagtgtc	180
actgctgatg	gccagggcga	cactgttggt	cctgatgctc	caaattgtaa	gggtgcaccc	240
acggagacgc	agccaattca	gtcgaccgcg	tctcatggcg	agcgcgctac	ttctcagccc	300
gaacagcagc	gccacaaga	tgaatccagc	tggattcaca	ttcgcgctgt	aatttctagc	360
caggaaagctg	ccacagtcac	tggcaagggt	ggagaaaacg	tatctcagat	tcgtcgtttg	420
tctggagcaa	agtgcactgt	cagcgactac	tcccgtgggtg	cagtcgaacg	tattttgacc	480
gtgagcggcc	cacaggatgc	cgttgccaag	gcgtttgggt	tgatcatccg	tacattgaac	540
aatgaacctc	ttgatgcccc	ctctaccgcc	caatccaaga	cataccctct	gcgtttgctg	600
atcccccatc	tccttatttg	ctccatcatt	ggcaaagggtg	gttcacgcat	tcgcgaaatt	660
caggaaagctt	ctggtgcccc	actgaatgca	tccgattcgt	gccttccctt	gtcctctgag	720
cgttcacttg	taattctcgg	cgttgcccgt	tctgtccaca	tcgctacctc	ctacgtcgcc	780
gtaaccctcg	ttgagcagct	cactgagcgc	tttgagggtc	ctgcagcctc	agcttatgcc	840
actcgacgcg	gtggccctgc	tggagcagtg	cctggcggta	tgcaggttgt	cccgtatggt	900
ccacagcccc	ctggtggtca	atatggccat	ccagaacatt	tcaagagaca	ccatcaccac	960
cccaatcgcg	ctgctgcagg	cgcttatggg	gtcccttacc	ttcacggtca	gcctgctccc	1020
gcaccagtgg	cccagccggc	tttgcatat	ggagctgctc	cccatgcccc	ttacgcagga	1080
gctggccccc	atcagcctgc	tccatacggc	gcaccgcagc	ccgctcaggc	acgcggcgct	1140
cctacccttg	ccacaccctg	tggaggtgtc	atgcctgggtc	agccattgac	tcagcagatc	1200
tacatcccca	acgacatggt	tggtgccatc	atcggaagag	gcggtgcgaa	gatcaatgag	1260
attcgacacc	tcagtggcag	tgtgatcaag	attaatgagc	ctcaagagaa	cagcaatgag	1320
cgtttggtga	ctattactgg	aacccaggaa	tgcaaccaaa	tggctctgta	catgctttac	1380
tcgcgacttg	gtag					1395

&lt;210&gt; 186

&lt;211&gt; 464

&lt;212&gt; PRT

<213> *Aspergillus fumigatus*

&lt;220&gt;

&lt;223&gt; Phylum CEA282.1; clone 10-4-20; contig 4929 region 328110-325663

Protein sequence

&lt;400&gt; 186

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Met Ser Ala Ser Pro Ser Ala Leu Gln Ser Thr Lys Arg Pro Leu Glu
1          5          10          15

Asp Pro Ser Ser Pro Ser Gly Pro Asn Asp Gln Pro Glu Ala Lys Arg
          20          25          30

Pro Ala Leu Asp Lys Val Val Lys Gly Asn Glu Ser Glu Thr Tyr Thr
          35          40          45

Asp Ala Lys Ala Glu Pro Ser Ala Ala Pro Ser Ala Thr Ala Asp Gly
          50          55          60

Gln Gly Asp Thr Val Val Pro Asp Ala Pro Asn Gly Lys Gly Ala Ser
65          70          75          80

Thr Glu Thr Gln Pro Ile Gln Ser Thr Ala Ser His Gly Glu Arg Ala
          85          90          95

Thr Ser Gln Pro Glu Gln Gln Arg Pro Gln Asp Glu Ser Ser Trp Ile
          100          105          110

His Ile Arg Ala Val Ile Ser Ser Gln Glu Ala Ala Thr Val Ile Gly
          115          120          125

Lys Gly Gly Glu Asn Val Ser Gln Ile Arg Arg Leu Ser Gly Ala Lys
          130          135          140

Cys Thr Val Ser Asp Tyr Ser Arg Gly Ala Val Glu Arg Ile Leu Thr
145          150          155          160

Val Ser Gly Pro Gln Asp Ala Val Ala Lys Ala Phe Gly Leu Ile Ile
          165          170          175

Arg Thr Leu Asn Asn Glu Pro Leu Asp Ala Pro Ser Thr Ala Gln Ser
          180          185          190

Lys Thr Tyr Pro Leu Arg Leu Leu Ile Pro His Leu Leu Ile Gly Ser
          195          200          205

Ile Ile Gly Lys Gly Gly Ser Arg Ile Arg Glu Ile Gln Glu Ala Ser
          210          215          220

Gly Ala Arg Leu Asn Ala Ser Asp Ser Cys Leu Pro Leu Ser Ser Glu
225          230          235          240

Arg Ser Leu Val Ile Leu Gly Val Ala Asp Ser Val His Ile Ala Thr
          245          250          255

Tyr Tyr Val Ala Val Thr Leu Val Glu Gln Leu Thr Glu Arg Phe Gly
          260          265          270

Gly Pro Ala Ala Ser Ala Tyr Ala Thr Arg Ser Gly Gly Pro Ala Gly
          275          280          285

Ala Val Pro Gly Gly Met Gln Val Val Pro Tyr Val Pro Gln Pro Ala
          290          295          300

Gly Gly Gln Tyr Gly His Pro Glu His Phe Lys Arg His His His His
305          310          315          320

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Pro Asn Arg Ala Ala Ala Gly Ala Tyr Gly Val Pro Tyr Leu His Gly  
                           325                          330                          335

Gln Pro Ala Pro Ala Pro Val Ala Gln Pro Ala Leu His Tyr Gly Ala  
                           340                          345                          350

Ala Pro His Ala Pro Tyr Ala Gly Ala Gly Pro His Gln Pro Ala Pro  
                           355                          360                          365

Tyr Gly Ala Pro Gln Pro Ala Gln Ala Arg Gly Ala Pro Thr Pro Ala  
                           370                          375                          380

Thr Pro Val Gly Gly Val Met Pro Gly Gln Pro Leu Thr Gln Gln Ile  
 385                          390                          395                          400

Tyr Ile Pro Asn Asp Met Val Gly Ala Ile Ile Gly Lys Gly Gly Ala  
                           405                          410                          415

Lys Ile Asn Glu Ile Arg His Leu Ser Gly Ser Val Ile Lys Ile Asn  
                           420                          425                          430

Glu Pro Gln Glu Asn Ser Asn Glu Arg Leu Val Thr Ile Thr Gly Thr  
                           435                          440                          445

Gln Glu Cys Asn Gln Met Ala Leu Tyr Met Leu Tyr Ser Arg Leu Gly  
                           450                          455                          460

&lt;210&gt; 187

&lt;211&gt; 2121

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> Phylum CEA282.2; clone 10-4-20; contig 4839 region 328075-330267  
 Genomic sequence containing 3' and 5'-ends and the coding region

&lt;400&gt; 187

taagttatcg	ccacggggaa	atagcccaaa	aggaaactcgt	cacagctgga	atcaacacca	60
agtaccgaag	aaacaagcga	gcagcggctg	tttggcttct	gcagctgcac	aaaaaatggg	120
aacgaagtga	atgaggttag	atagagatga	ggatggatca	agaagcgccc	tccagatgta	180
gcaatgaaga	gatgatgttg	caagaagagg	tgaacaagc	tggcggcacg	ggatcaggct	240
aggctagata	gggttagcaa	cgagggtgac	atcacgtgag	aacgggcac	gtgatatgga	300
tgacaattaa	catcataaac	actcttcgtt	cagttgctgt	gactcctgac	gcgtaagggg	360
atctgggggtg	aagtcaagca	atagactctc	tgacagattt	gacttttagag	aaagtaaata	420
acaccactat	ggacatctcg	caagaaaccg	ttgataaaat	acgacgtttc	gcgcaaaagc	480
gccaaaaagc	ggaggagttc	tacgaggaac	actcggtaaa	tccagctaata	tttgacgctt	540
acaatcgcaa	ggttgatgag	acgttggcag	agctgcaggc	tcaagtcaaa	cgatcatgagg	600
atgagctccg	caaggtacgt	caacaagttg	cctagaatat	aagccgactg	tcacaagaga	660
tttcatgcat	gaattaggaa	tactgacaag	aggaaacagc	acgcatgacc	accacgatcg	720
agttcgctca	aattggggca	gataccttggg	cccgcatctc	agaagtgcgc	agagccaaga	780
aagcgtatga	ttctcttctg	caatcggaag	cgcgactgcc	gagtccaggc	tcgcccttgc	840
cttcattact	tgcggttgac	gaggcgtctc	gtctcgtcaa	ggagagcaag	acctcaatct	900
cactgacggc	ggagaaactg	tctgcggatc	gtcagcgctt	gaaagcggaa	gaagccaatt	960
tgcgcgatgc	gcaactgatc	aaagacgggt	tggagaaaag	gattgagcgg	ctgaacgcag	1020
aaaaatcgag	tcaagtccag	aaaactcctg	cgcagcttgc	gtatgatctc	gtcaaggagc	1080
agcaggaaaa	gatcgagaga	cttgataacta	ccacagaaga	gctaaagtcc	tctctctata	1140
aatttgcga	agacacactt	gccccaatgc	ttgctgcaga	aaatctgggc	gggtcccactg	1200
tcgggatgc	gttggaaaatt	tcggacacta	ccttaaaagc	gggctacact	agccatggga	1260
agcctaagaa	accaaaaact	ccggccgtgg	ggacttctga	cagtggccaa	cagcggattg	1320
acgagcttgt	tcgtcgccaa	actgcgcagg	agggcaacga	gcaggcaacc	cttttgaaca	1380

```

aaagagagggc ggccgcccgt gaaatgcgag ctcttcttac tgctctgtta gatgcggatt 1440
actcctatgt cgaccttccg cactgagtcag cggcctcgcg ctttctagta agagcgaagg 1500
tagctcaatt ccattccgcg gatgccagga agcttcgggt aattgatttt gggcgctcat 1560
tagtcgattg aggtggctac atgtaccgta ctacatctcc cagcttacaa atggtatcac 1620
atttcaccaa acatctggga aaagacaaac agacgccatc cccacggata tatagcgact 1680
caaccgaaaag ccagtaagat atctagagcc ggcgaaaacc acgtgtttca acgaagaagc 1740
ggccccgaaa gccactggta gcataacgcc ttgagaatgc gagagataca tcaaaagctt 1800
atcagaaaagt tcaatgctcg aggtcaaaaa tataccgtta atgccataca agaaacatgg 1860
aagaagaaaag accgtagccg ggtatcagat cggcatcatt ccgatgctgg tagaagtact 1920
cttgggccgta ttctttgctt tggagccagt tcgggaaccc gccgagcgct tgttgacttg 1980
atcgctgggc tcccttctag gtcgcggcgt ttttattttt gaactcgacc ctgtagcggt 2040
cttgcggtgg aagcgcttct tggacgaagt ctttcttttc ttggaacggc tagtctcggt 2100
gtcttcatac tcttcggatg a 2121

```

<210> 188

<211> 1143

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.2; clone 10-4-20; contig 4839 region 328075-330267  
Genomic sequence containing the coding region

<400> 188

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gcggaggagt tctacgagga aactcggta aatccagcta attttgacgc ttacaatcgc 120
aagttggatg agacgttggc agagctgcag gctcaagtca aacgtcatga ggatgagctc 180
cgcaaggtac gtcaacaagt tgccatgaat ataagccgac tgtcacaaga gatttcatgc 240
atgaattagg aatactgaca agaggaacag ctacgcataa ccaccacgat cgagttcgct 300
caaattgggg cagatccttg ggcccgcatc tcagaagtgc gcagagccaa gaaagcgtat 360
gattctcttc tgcaatcgga aacgcgactg ccgagtccag gctcgccctt gccttcatta 420
cttgcggttg acgaggcgct tcgtctcgct aaggagagca agacctcaat ctactgacg 480
gcggagaaaac tgtctgcgga tcgtcagcgc ttgaaagcgg aagaagccaa tttgcgcgat 540
gcgcaactga tcaaagacgg gttggagaaa aggattgagc ggctgaacgc agaaaaatcg 600
agtcaagtcc agaaaactcc tgcgcagctt gcgtatgatc tcgtcaagga gcagcaggaa 660
aagatcgaga gacttgatac taccacagaa gagctaaagt cctctctcta taaatttgct 720
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gttcgctgcc aaactgcgca ggagggcaac gagcaggcaa cccttttgaa caaaagagag 960
gcggccgccc ctgaaatgcg agctcttctt actgctctgt tagatgcgga ttactcctat 1020
gtcgaccttc cgcacgagtc agcggcctcg cgctttctag taagagcgaa ggtagctcaa 1080
ttccatccgc gcgatgccag gaagcttcgg ttaattgatt ttgggcgctc attagtcgat 1140
tga 1143

```

<210> 189

<211> 1035

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.2; clone 10-4-20; contig 4839 region 328075-330267  
Coding region without exons

<400> 189

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gcggaggagt tctacgagga aactcggta aatccagcta attttgacgc ttacaatcgc 120
aagttggatg agacgttggc agagctgcag gctcaagtca aacgtcatga ggatgagctc 180
cgcaagttcg ctcaaattgg ggcagatcct tgggcccgca tctcagaagt gcgcagagcc 240

```



```

aagaaagcgt atgattctct tctgcaatcg gaaacgcgac tgccgagtc aggctcgccc 300
ttgccttcat tacttgcggt tgacgaggcg tctcgtctcg tcaaggagag caagacctca 360
atctcactga cggcggagaa actgtctgcg gatcgtcagc gcttgaaagc ggaagaagcc 420
aatttgcgcg atgcgcaact gatcaaagac gggttggaga aaaggattga gcggtgaac 480
gcagaaaaat cgagtcaagt ccagaaaaact cctgcgcagc ttgcgtatga tctcgtcaag 540
gagcagcagg aaaagatcga gagacttgat actaccacag aagagctaaa gtcctctctc 600
tataaatttg tcgaagacac acttgcccca atgcttgctg cagaaaatct gggcgggtccc 660
actgtcggag atgcgttgga aatttcggac actaccttaa aagcgggcta cactagccat 720
gggaagccta agaaaccaa aactccggcc gtggggactt ctgacagtgg ccaacagcgg 780
attgacgagc ttgttcgctg ccaaactgcg caggagggca acgagcaggc aacccttttg 840
aacaaaagag aggcggccgc cgctgaaatg cgagctcttc ttactgctct gttagatgcg 900
gattactcct atgtcgacct tccgcacgag tcagcggcct cgcgctttct agtaagagcg 960
aaggtagctc aattccatcc gcgcgatgcc aggaagcttc ggttaattga ttttgggcgc 1020
tcattagtcg attga 1035

```

<210> 190

<211> 344

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA282.2; clone 10-4-20; contig 4839 region 328075-330267  
Protein sequence

<400> 190

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Met Asp Ile Ser Gln Glu Thr Val Asp Lys Ile Arg Arg Phe Ala Gln
1           5           10           15

```

```

Lys Arg Gln Lys Ala Glu Glu Phe Tyr Glu Glu His Ser Val Asn Pro
20           25           30

```

```

Ala Asn Phe Asp Ala Tyr Asn Arg Lys Leu Asp Glu Thr Leu Ala Glu
35           40           45

```

```

Leu Gln Ala Gln Val Lys Arg His Glu Asp Glu Leu Arg Lys Phe Ala
50           55           60

```

```

Gln Ile Gly Ala Asp Pro Trp Ala Arg Ile Ser Glu Val Arg Arg Ala
65           70           75           80

```

```

Lys Lys Ala Tyr Asp Ser Leu Leu Gln Ser Glu Thr Arg Leu Pro Ser
85           90           95

```

```

Pro Gly Ser Pro Leu Pro Ser Leu Leu Ala Val Asp Glu Ala Ser Arg
100          105          110

```

```

Leu Val Lys Glu Ser Lys Thr Ser Ile Ser Leu Thr Ala Glu Lys Leu
115          120          125

```

```

Ser Ala Asp Arg Gln Arg Leu Lys Ala Glu Glu Ala Asn Leu Arg Asp
130          135          140

```

```

Ala Gln Leu Ile Lys Asp Gly Leu Glu Lys Arg Ile Glu Arg Leu Asn
145          150          155          160

```

```

Ala Glu Lys Ser Ser Gln Val Gln Lys Thr Pro Ala Gln Leu Ala Tyr
165          170          175

```

```

Asp Leu Val Lys Glu Gln Gln Glu Lys Ile Glu Arg Leu Asp Thr Thr
180          185          190

```

Thr Glu Glu Leu Lys Ser Ser Leu Tyr Lys Phe Val Glu Asp Thr Leu  
 195 200 205  
 Ala Pro Met Leu Ala Ala Glu Asn Leu Gly Gly Pro Thr Val Gly Asp  
 210 215 220  
 Ala Leu Glu Ile Ser Asp Thr Thr Leu Lys Ala Gly Tyr Thr Ser His  
 225 230 235 240  
 Gly Lys Pro Lys Lys Pro Lys Thr Pro Ala Val Gly Thr Ser Asp Ser  
 245 250 255  
 Gly Gln Gln Arg Ile Asp Glu Leu Val Arg Arg Gln Thr Ala Gln Glu  
 260 265 270  
 Gly Asn Glu Gln Ala Thr Leu Leu Asn Lys Arg Glu Ala Ala Ala Ala  
 275 280 285  
 Glu Met Arg Ala Leu Leu Thr Ala Leu Leu Asp Ala Asp Tyr Ser Tyr  
 290 295 300  
 Val Asp Leu Pro His Glu Ser Ala Ala Ser Arg Phe Leu Val Arg Ala  
 305 310 315 320  
 Lys Val Ala Gln Phe His Pro Arg Asp Ala Arg Lys Leu Arg Leu Ile  
 325 330 335  
 Asp Phe Gly Arg Ser Leu Val Asp  
 340

<210> 191

<211> 2000

<212> DNA

<213> *Aspergillus fumigatus*

<220>

<223> Phylum CEA283; clone 11-6-20; contig 4910 region 9638-11637  
 Genomic sequence containing 3' and 5'-ends and the coding region

<400> 191

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cttctcacct	ctgctccttt	aatacttcat	tgcggggata	ttattccgtg	ctggacagct	120
tctgcaagat	cagtaattat	gtaggaacac	gaaaacaatg	ttctacacat	tagttttctc	180
ctgatgacca	tcttctcttt	gatcaatgca	gcagacaaca	aatcctgtcc	aatcatccca	240
acatactgtt	tcctaccttg	attggcgcaa	atccggcgac	aataatcaag	ggtagagtga	300
tggactaggc	tcaggcggtt	tgactttgca	aatccaattg	aattctgata	agtgtctaac	360
cgatgatggc	gttgagcgac	caaggacaat	ttccgactga	gctcagcatt	tcctctgctc	420
gcgactcgcg	aggcgcggtc	caggacggga	ggtcttggaa	aggctgaacg	gtcaatcaat	480
catcaaatgg	gtaggatggt	gcgtaaatag	cccacatgcg	cataaaaagt	gatgagtgcc	540
gcatacggtat	cttcgttctt	gtttcctttt	ccgtctcacc	ccaagatcat	gggtcatgaa	600
ttgataatag	tatcgtcaac	tggttttagc	tgatgactac	gtatcttttt	gagcgtcaag	660
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tattctgata	tttcagttca	ataatcgaaa	aatagtgacg	cgcggtatgg	tgcatagctt	900
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tatgatgata	cggccgcata	cgacctctaa	ttcatcgaaat	actccagaag	cggctagcca	1020
ctttcctgaa	atcgaggtct	atccatggac	tcagcatctt	gtacggagta	caaactcctg	1080
ccagcttatt	ccaactgatg	accctggccc	ttatatgagc	aagcaggata	tgattgggag	1140
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agctattgtc	tcacacaggt	atgcactgcg	gaacatggat	taattgatac	ttatgaaccc	1260
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cgcgtctgta	catcttgacc	tccttcggcc	tctcctttgc	gctgtgctca	gttttccctt	1980
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&lt;210&gt; 192

&lt;211&gt; 4336

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

&lt;223&gt; ATPase; Phylum CEA284.1; clone 4-3-4; contig 4899

region 472441-476776

Genomic sequence containing 3' and 5'-ends and the coding region

&lt;400&gt; 192

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cggcaaatgc	tcgcgcaccg	acccacggaa	ttcggccaag	attctggatc	gattgccctt	180
tatgtatgcg	aaggtttggg	gatgtgattg	gtgtgcagcg	taaacgagta	cggattgata	240
agagtgccaa	gatttgaacc	actgttcacg	tcatggaggg	gggtttccgg	cacgccgggt	300
aggagtgaga	cagagtgact	taaatatgtc	gcgatacccc	cgcaacgacg	ggagaagaaa	360
atctggttct	acaacctagg	ctttaatttc	caagttgatt	tcaagtcggt	gtgtatggac	420
tctcactcgc	ttgaagatac	gatatacatg	aagcctcctt	aggataactg	caactggaata	480
gaacattttc	gttatataac	atgggtgctc	agaagaagca	atcctctgat	aactctcagg	540
ctttgtctca	gcctgctcat	gcgcttcgct	atgaggatgt	ccttcgtgag	ctggccgctc	600
atccagacca	gggtctgacc	gtgggggagg	cgaagcgaag	actccaacaa	tatggtccga	660
atgaactgga	agggggagag	ggtgtttcca	ttgtcaagat	tgtcattagg	cagatcgcaa	720
atgccatgat	gctggttagt	ctctcccttt	tgtagacag	acaacgacag	acaactgacg	780
acagcaggtc	ctgatcatcg	ccatggcggt	cagtttcggc	attcaatcct	ggattgaggg	840
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tgggaatcaa	cgttggcaca	ccgctgcagc	gcaaactctc	gaaactggct	ttggcccttt	1500
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ttccagccaa	catggacagt	cttgccaaag	atgttgcgga	cgccatgggtg	atgactgcca	2640
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ttgctcgggtg	cgctcccaac	acaaagggtc	ggatgattga	tgccttcat	cgtcgggggtc	2760
ggtttgcggc	aatgactggt	gatggagtca	atgactcgcc	atcgttgaag	cgggcagatg	2820
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&lt;210&gt; 193

&lt;211&gt; 3336

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> ATPase; Phylum CEA284.1; clone 4-3-4; contig 4899  
region 472441-476776

Genomic sequence containing the coding region

&lt;400&gt; 193

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&lt;210&gt; 194

&lt;211&gt; 3180

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> ATPase; Phylum CEA284.1; clone 4-3-4; contig 4899  
region 472441-476776

Coding region without exons

&lt;400&gt; 194

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&lt;210&gt; 195

&lt;211&gt; 1059

&lt;212&gt; PRT

<213> *Aspergillus fumigatus*

&lt;220&gt;

<223> ATPase; Phylum CEA284.1; clone 4-3-4; contig 4899  
region 472441-476776

## Protein sequence

&lt;400&gt; 195

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Val Asp Pro Asp Gln Gly Leu Thr Val Gly Glu Ala Lys Arg Arg Leu
35      40      45
Gln Gln Tyr Gly Pro Asn Glu Leu Glu Gly Gly Glu Gly Val Ser Ile
50      55      60
Val Lys Ile Val Ile Arg Gln Ile Ala Asn Ala Met Met Leu Val Leu
65      70      75      80
Ile Ile Ala Met Ala Val Ser Phe Gly Ile Gln Ser Trp Ile Glu Gly
85      90      95
Gly Val Ile Gly Ala Val Ile Gly Leu Asn Ile Val Val Gly Val Tyr
100     105     110
Gln Asp Tyr Ala Ala Glu Lys Thr Met Asp Ser Leu Arg Ser Leu Ser
115     120     125
Ser Pro Thr Gly Thr Val Thr Arg Asp Gly Lys Thr Ser Thr Ile Pro
130     135     140
Ala Asn Glu Ile Val Pro Gly Asp Met Ile Glu Leu Lys Val Gly Asp
145     150     155     160
Thr Val Pro Ala Asp Leu Arg Leu Val Asp Ala Met Asn Phe Glu Thr
165     170     175
Asp Glu Ala Leu Leu Thr Gly Glu Ser Leu Pro Val Gln Lys Glu Val
180     185     190
Asp Thr Thr Phe Asp Pro Asp Thr Gly Pro Gly Asp Arg Leu Asn Ile
195     200     205
Ala Tyr Ser Ser Ser Thr Val Thr Arg Gly Arg Ala Arg Gly Val Val
210     215     220
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225     230     235     240
Arg Ala Ser Asp Ser Lys Arg Arg Pro Val Lys Arg Gly Pro Glu Gly
245     250     255
Glu Thr Lys Lys Arg Trp Tyr Val Gln Ala Trp Thr Leu Thr Cys Thr
260     265     270
Asp Ala Val Gly Arg Phe Leu Gly Ile Asn Val Gly Thr Pro Leu Gln
275     280     285
Arg Lys Leu Ser Lys Leu Ala Leu Ala Leu Phe Ala Ile Ala Ile Ile
290     295     300

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Phe Ala Ile Ile Val Met Gly Val Asn Gly Phe Arg Asn Asp Lys Glu  
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 325 330 335  
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 340 345 350  
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 355 360 365  
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 370 375 380  
 Gly Arg Met Val Ala Lys Arg Ala Trp Ile Pro Ser Val Gly Thr Phe  
 385 390 395 400  
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 405 410 415  
 Ser Leu Leu Pro Asp Pro Pro Val Lys Val Gly Pro Asp Ala His Gly  
 420 425 430  
 Glu Pro Ser Arg Pro Glu Asp Leu Leu Lys Asp Asn Pro Leu Leu Glu  
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 Gln Tyr Leu Asn Val Ala Ala Met Ala Asn Leu Ala His Val His Arg  
 450 455 460  
 Ser Glu His Asn Glu Trp Gln Ala Arg Gly Glu Pro Thr Asp Ile Ala  
 465 470 475 480  
 Ile Gln Val Phe Ala Ser Arg Phe Asn Trp Gly Arg Asp Arg Trp Thr  
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 Lys Gly Glu Lys Pro Val Trp Arg Gln Lys Ala Glu Tyr Pro Phe Asp  
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 Ser Thr Val Lys Lys Met Ser Val Ile Phe Lys Asn Thr Asn Asp Asp  
 515 520 525  
 Arg Glu Met Ile Phe Thr Lys Gly Ala Val Glu Arg Val Ile Glu Ala  
 530 535 540  
 Cys Thr Thr Val Thr Trp Thr Ala Gly Ser Asp Pro Ile Ala Leu Asp  
 545 550 555 560  
 Glu Asn Ile Lys Glu Glu Ile Leu Gln Asn Met Glu Ala Leu Ala Lys  
 565 570 575  
 Glu Gly Leu Arg Val Leu Cys Leu Ala Cys Arg Glu Asn His Asn Pro  
 580 585 590  
 Val Lys Gly Glu Val Val Pro Ala Arg Glu Glu Val Glu Lys Asp Leu  
 595 600 605  
 Thr Phe Cys Gly Leu Ile Gly Leu Tyr Asp Pro Pro Arg Pro Glu Thr  
 610 615 620  
 Ala Gly Ala Ile Asp Glu Cys Tyr Arg Ala Gly Ile Ser Val His Met



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Gly Ile Ile Pro Ala Asn Met Asp Ser Leu Ala Lys Asp Val Ala Asp						
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Ala Met Val Met Thr Ala Ser Gln Phe Asp Lys Leu Thr Asp Glu Glu						
		675		680		685
Ile Asp Ala Leu Pro Thr Leu Pro Ala Val Ile Ala Arg Cys Ala Pro						
		690		695		700
Asn Thr Lys Val Arg Met Ile Asp Ala Leu His Arg Arg Gly Arg Phe						
		705		710		715
Ala Ala Met Thr Gly Asp Gly Val Asn Asp Ser Pro Ser Leu Lys Arg						
		725		730		735
Ala Asp Val Gly Ile Ala Met Gly Gln Ser Gly Ser Asp Val Ala Lys						
		740		745		750
Asp Ala Ser Glu Leu Val Leu Thr Asp Asp Asn Phe Ala Ser Ile Ile						
		755		760		765
Asn Gly Ile Glu Glu Gly Arg Arg Ile Phe Asp Asn Ile Gln Lys Phe						
		770		775		780
Val Leu His Leu Leu Ala Glu Asn Val Gly Leu Ala Leu Thr Leu Leu						
		785		790		795
Ile Gly Leu Cys Phe Lys Asp Asp Asn Gly Gln Ser Val Phe Pro Ile						
		805		810		815
Ala Pro Val Glu Ile Leu Trp Ile Ile Met Ile Thr Ser Gly Leu Pro						
		820		825		830
Asp Met Gly Leu Gly Met Glu Ile Ala Ala Pro Asp Ile Met Asp Arg						
		835		840		845
Pro Pro Gln Ser Val Ser Ile Phe Thr Trp Glu Val Ile Val Asp Thr						
		850		855		860
Met Val Tyr Gly Val Trp Met Ala Ala Leu Cys Leu Ala Ser Phe Ser						
		865		870		875
Leu Val Leu Phe Gly Trp Gly Asp Gly Asn Leu Ala Ser Gly Cys Asn						
		885		890		895
Ser Asp Tyr Ser Pro Glu Cys Asp Gly Val Phe Arg Ala Arg Ala Thr						
		900		905		910
Thr Phe Val Cys Met Thr Trp Phe Ala Leu Phe Leu Ala Trp Glu Met						
		915		920		925
Ile Asp Met Arg Arg Ser Phe Phe Arg Met Gln Pro Asn Ser Lys Arg						
		930		935		940
Tyr Phe Thr Gln Trp Met Phe Asp Val Trp Arg Asn Lys Phe Leu Phe						
		945		950		955
						960

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Trp Gly Val Val Phe Val Glu Ala Ile Leu Phe Phe Ala Gly Cys Glu  
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Ala Trp Lys Trp Cys Lys Arg Ile Tyr Phe Arg His Thr Ser Gln  
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Lys Glu Thr Gly Arg Glu Arg Val Leu Arg Asp Phe Ser Arg Tyr  
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Val Glu Lys Ser Met Val  
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&lt;210&gt; 196

&lt;211&gt; 2059

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

&lt;223&gt; Homologue GmZnf1; Phylum CEA284.2;

contig 4899 region 477626-479684

Genomic sequence containing 3' and 5'-ends and the coding region

&lt;400&gt; 196

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&lt;210&gt; 197

&lt;211&gt; 1059

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

&lt;223&gt; Homologue GmZnf1; Phylum CEA284.2;

contig 4899 region 477626-479684

Genomic sequence containing the coding region

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&lt;210&gt; 198

&lt;211&gt; 1059

&lt;212&gt; DNA

<213> *Aspergillus fumigatus*

&lt;220&gt;

&lt;223&gt; Homologue GmZnf1; Phylum CEA284.2;

contig 4899 region 477626-479684

Coding region without exons

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<210> 199

<211> 352

<212> PRT

<213> *Aspergillus fumigatus*

<220>

<223> Homologue GmZnf1; Phylum CEA284.2;  
contig 4899 region 477626-479684  
Protein sequence

<400> 199

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Thr Met Ser His Pro Asp Leu Ser Thr Ile Leu Glu Val Tyr Pro Glu
35          40          45
Cys Glu Val Thr Cys Tyr Gly Tyr Ala Pro Ser Gln Arg Arg Arg Cys
50          55          60
Arg Met Arg Thr Arg Lys Asp Asn Arg Asp Arg Ala Ser Tyr Leu Leu
65          70          75          80
Glu Glu Gly Thr Arg Tyr Leu Gln Arg Gly Leu Pro Val Asp Gly Leu
85          90          95
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100         105         110
Gln Ala Asp Asp Leu Val Arg Asp Trp Arg Ala Lys Leu Arg Glu Phe
115         120         125
Gln Gln Gln Thr Leu Leu Asn Ala Met Leu Lys Ser Leu Gln Glu Leu
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Leu Pro Glu Arg Val Ser Ser Pro Thr Arg Leu Glu Arg Ser Ala Ala
165         170         175
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180         185         190
Glu Glu Arg Gly Asp Arg Glu Asp Glu Pro Glu Pro Glu Pro Glu Pro
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Cys	Pro	Leu	Arg	Glu	Gln	Asp	Ser	Asp	Glu	Asn	Gly	Glu	Gly	Ser	Glu
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Ile	Asp	Val	Trp	His	Ala	Thr	Gln	Arg	Thr	Phe	Glu	Thr	Pro	Arg	Gly
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